

NAME OF THE DOCUMENT

PATENT SPECIFICATION

EXHIBIT

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TITLE OF THE INVENTION NEW GENES

DETAILED EXPLANATION OF THE INVENTION

CLAIMS:

1. A purified and isolated protein selected from the group consisting of:

(a) a protein which consists of an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178; and

(b) a protein that activates NF- κ B (Nuclear factor kappa B) and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178.

2. A purified and isolated protein that activates NF- κ B and comprises an amino acid sequence having at least 95% identity to the protein according to claim 1 over the entire length thereof.

3. An isolated polynucleotide which comprises a nucleotide sequence encoding a protein selected from the group consisting of:

(a) a protein which comprises an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or

178; and

(b) a protein that activates NF- κ B and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178.

4. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence represented by SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177; and a polynucleotide sequence complementary to said polynucleotide sequence;

(b) a polynucleotide sequence encoding a protein that activates NF- κ B and hybridizing with a polynucleotide having the polynucleotide sequence of (a) under stringent conditions; and

(c) a polynucleotide sequence which encodes a protein that activates NF- κ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177.

5. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to claim 3 over the entire length thereof.

6. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to claim 4 over the entire length thereof.
7. A purified and isolated protein encoded by the polynucleotide according to any one of claims 3 to 6.
8. A recombinant vector which comprises a polynucleotide according to any one of claims 3 to 6.
9. A transformed cell which comprises the recombinant vector according to claim 8.
10. A membrane of the cell according to claim 9, when the protein according to claim 1 or 2 is a membrane protein.
11. A process for producing a protein comprising,
 - (a) culturing a transformed cell comprising the isolated polynucleotide according to any one of claims 3 to 6 under conditions providing expression of the encoded protein; and
 - (b) recovering the protein from the culture.
12. A process for diagnosing a disease or susceptibility to a disease in a subject related to expression or activity of the protein of claim 1, 2 or 7 in a subject comprising:
 - (a) determining the presence or absence of a mutation in the nucleotide sequence encoding said protein in the genome of said subject; and/or
 - (b) analyzing the amount of expression of said protein in a sample derived from said subject,wherein a diagnosis of disease is made when the amount of the protein expressed is more than 2-fold or higher than normal, or half or lower than normal.
13. A method for screening compounds in respect of activity to inhibit or promote NF- κ B activation, which comprises the steps of:
 - (a) providing a cell with a gene encoding a protein that activates NF- κ B, and a component that provides a detectable signal associated with activation of NF- κ B;
 - (b) culturing a transformed cell under conditions, which permit the expression of the gene in a transformed cell;
 - (c) contacting the transformed cell with one or more compounds;

(d) measuring the detectable signal; and

(e) isolating or identifying as an activator compound a compound that increases said detectable signal 2-fold or higher than normal and/or isolating or identifying as an inhibitor compound a compound that decreases said detectable signal half or lower than normal.

14. A process for producing a pharmaceutical composition, which comprises the steps of:

(a) providing a cell with a gene encoding a protein that activates NF- κ B, and a component capable of providing a detectable signal;

(b) culturing a transformed cell under conditions, which permit the expression of the gene in the transformed cell;

(c) contacting the transformed cell with one or more compounds;

(d) measuring the detectable signal;

(e) isolating or identifying as an activator compound a compound that increases said detectable signal 2-fold or higher than normal and/or isolating or identifying as an inhibitor compound a compound that decreases said detectable signal half or less than normal; and

(f) optimizing the isolated or identified compound as a pharmaceutical composition.

15. A kit for screening a compound in respect of activity to inhibit or promote NF- κ B activation, which comprises:

(a) a cell comprising a gene encoding a protein that activates NF- κ B, and a component that provides a detectable signal upon activation of NF- κ B; and

(b) reagents for measuring the detectable signal.

16. A monoclonal or polyclonal antibody that specifically binds to the protein according to claim 1, 2 or 7.

17. A process for producing a monoclonal or polyclonal antibody that specifically binds to the protein according to claim 1, 2 or 7, which comprises administering the protein according to claim 1, 2 or 7 or epitope-bearing fragments thereof to a non-human animal.

18. An antisense oligonucleotide complementary to the polynucleotide according to any one of claims 3 to 6, which prevents NF- κ B activator protein expression.

19. A ribozyme which inhibits NF- κ B activation by cleavage of RNA that encodes

the protein according to claim 1, 2 or 7, or by cleavage of RNA that encodes some protein of the pathway that leads to I κ B (Inhibitory protein of NF- κ B) degradation.

20. A method for treating a disease, which comprises administering to a subject an amount of a compound screened by the process according to claim 13, and/or a monoclonal or polyclonal antibody according to claim 16, and/or an antisense oligonucleotide according to claim 18 and/or a ribozyme according to claim 19 effective to treat a disease selected from the group consisting of inflammation, autoimmune diseases, infectious disease and cancers.

21. A pharmaceutical composition produced by the process according to claim 14 as an inhibitor or promoter of NF- κ B activation.

22. A pharmaceutical composition according to claim 21 for the treatment of inflammation, autoimmune diseases, cancers or viral infections.

23. A method of treating inflammation, autoimmune diseases, cancers and viral infections, which comprises administering a pharmaceutical composition produced by the process according to claim 14 to a patient suffering from a disease associated with NF- κ B activation.

24. A pharmaceutical composition according to claim 21 for the treatment of GVHD, dermatosis, IgA nephritis, purpuric nephritis, proliferative nephritides, or fulminant hepatitis.

25. A method of treating GVHD, dermatosis, IgA nephritis, purpuric nephritis, proliferative nephritides, or fulminant hepatitis, which comprises administering a pharmaceutical composition produced by the process according to claim 14 to a patient suffering from a disease associated with inhibition of NF- κ B.

26. A pharmaceutical composition which comprises a monoclonal or polyclonal antibody according to claim 16 as an active ingredient.

27. A pharmaceutical composition which comprises an antisense oligonucleotide according to claim 18 as an active ingredient.

28. The pharmaceutical composition according to claim 26 or 27, wherein the target disease is selected from the group consisting of inflammation, autoimmune diseases,

infectious diseases and cancers.

29. A method for obtaining a novel gene having a function, which comprises at least the following steps:

- (a) constructing a full-length cDNA library by the oligo-capping method;
- (b) cotransfecting the full-length cDNA and a plasmid containing a factor emitting a signal indicative of the presence of a protein having the function into cells; and
- (c) selecting a plasmid emitting the signal.

30. A computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178.

31. A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to claim 30 with data of said other nucleotide sequences and/or amino acid sequences.

32. An insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173,

175 and 177, are fixed.

33. An insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178, are fixed.

DETAILED EXPLANATION OF THE INVENTION

TECHNICAL FIELD OF THE INVENTION

The present invention relates to a protein capable of activating NF- κ B, a DNA sequence encoding the protein, a method for obtaining the DNA, a recombinant vector containing the DNA, a transformant containing the recombinant vector, and an antibody which specifically reacts with the protein. The present invention also relates to use of the protein, DNA molecule or antibody of the invention in the diagnosis, treatment or prevention of diseases associated with the excessive activation or inhibition of NF- κ B.

The present invention also relates to a method for screening a substance capable of inhibiting or promoting NF- κ B activation by using the protein, DNA, recombinant vector and transformant.

DESCRIPTION OF THE RELATED ART

The transcription factor NF- κ B (nuclear factor kappa B) plays an important role in the transcriptional regulation of various genes involved in inflammation and immunological reactions. NF- κ B is a homo- or heterodimer which belongs to the Rel family. In unstimulated conditions, NF- κ B normally resides in the cytoplasm as an inactive form by forming a complex with an I κ B inhibitory protein (Inhibitory protein of NF- κ B) to mask the nuclear transport signal of NF- κ B.

When cytokines such as interleukin (IL)-1 and tumor necrosis factor (TNF)- α stimulate cells, I κ B is phosphorylated by IKK (I κ B kinase) and degraded by the 26S

proteasome through ubiquitination. The released NF- κ B moves to the nucleus, where it binds to the DNA sequence called the NF- κ B binding sequence and induces the transcription of the gene, which is under control of NF- κ B is believed to regulate the expression of genes such as those for immunoglobulins, inflammatory cytokines (e.g., IL-1 and TNF- α), interferons and cell adhesion factors. NF- κ B is involved in inflammation and immune responses through the expression induction of these genes.

The inhibition of the function or activation of NF- κ B may inhibit the expression of many factors (proteins) involved in inflammatory or immunological diseases or other diseases such as tumor proliferation. Thus, NF- κ B is a promising target for medicaments against diseases caused or characterized by autoimmunity or inflammation [see e.g., Clinical Chemistry 45, 7-17 (1999); J Clin. Pharmacol. 38, 981-993 (1998); Gut 43, 856-860 (1998); The New England Journal of Medicine 366, 1066-1071 (1997); TiPS 46-50 (1997); The FASEB Journal 9, 899-909 (1995); Nature 395, 225-226 (1998); Science 278, 818-819 (1997); Cell 91, 299-302 (1997)].

Extracellular information is converted into a certain signal, which passes through the cell membrane and goes through the cytoplasm to the nucleus, where it regulates the expression of the target gene and causes cell responses. Therefore the elucidation of the mechanism of intracellular signal transduction from extracellular stimuli to NF- κ B activation is of very important significance, because it provides very important means of developing new medicaments or therapies against autoimmune diseases and diseases exhibiting inflammatory symptoms.

It is believed that the signal transduction pathway from certain cell stimulation to NF- κ B activation includes many steps mediated by various transmitters such as protein kinases. Therefore it is desirable for more efficient drug discovery to identify the transmitters which play a key role in the pathway, and to focus research on the transmitters to establish a new drug-screening method. Some signaling molecules involved in NF- κ B activation have been identified [e.g., IKK, ubiquitination enzymes and the 26S proteasome described above, as well as TNF receptor associated factor 2 (TRAF2) and NF- κ B inducing kinase (NIK)]. However, most of the mechanism of NF- κ B activation remains

unknown, and it has been desired new signaling molecules to be identified and further the NF- κ B activation mechanism to be elucidated.

PROBLEM TO BE SOLVED BY THE INVENTION

The object of the present invention is to identify a new gene and protein capable of activating NF- κ B, and to provide a method of use of them in medicaments, diagnostics and therapy. That is, the present invention provides a new protein capable of activating NF- κ B, a DNA sequence encoding the protein, a recombinant vector containing the DNA, a transformant containing the recombinant vector, a process for producing the protein, an antibody directed against the protein or a peptide fragment thereof, and a process for producing the antibody.

The present invention also provides a method for screening a substance capable of inhibiting or promoting NF- κ B activation, a kit for the screening, a substance capable of inhibiting or promoting NF- κ B activation obtainable by the screening method or the screening kit, a process for producing the substance, a pharmaceutical composition containing a substance capable of inhibiting or promoting NF- κ B activation, etc.

MEANS TO SOLVE THE PROBLEM

Recently, random analysis of cDNA molecules has been intensively carried out to analyze various genes, which are expressed in vivo. The cDNA fragments thus obtained have been entered for databases and published as ESTs (Expressed Sequence Tags, e.g., <http://www.ncbi.nlm.nih.gov/dbEST>). However, ESTs are merely sequence information, and it is difficult to predict their functions. ESTs are also arranged in UniGene (<http://www.ncbi.nlm.nih.gov/UniGene>), and about 92,000 clusters have been registered until now. However, most of these ESTs have their 5' end nucleotide sequences deleted, and contain no translation initiation site. Therefore it is unlikely that such analysis will directly lead to gene functional analysis such as the analysis of protein functions on the assumption of the determination of mRNA coding regions and the understanding of gene expression control by the analysis of promoters.

On the other hand, one method to elucidate functions of gene products (i.e., proteins) is transient expression cloning method using animal cells [see e.g., "Idenshi

Kougaku Handbook (Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.]. This method involves transfecting animal cells with a cDNA library constructed using an animal cell expression vector to directly express a functional protein, and identifying and cloning the cDNA based on the biological activity of the protein having an effect on the cells. This method requires no chemical information (amino acid sequences and molecular weights) regarding the target protein product as a prerequisite, and allows the identification of cDNA clones by detecting specific biological activity of the protein expressed in the cells or culture.

For the efficient expression cloning, there is a need to devise a method of preparing a cDNA library. Several methods have been widely used to construct cDNA libraries [e.g., the method of Gubbler-Hoffman: *Gene* 25 (1983); and the method of Okayama-Berg: *Mol. Cell. Biol.* 2 (1982)]. However, most of the cDNA molecules prepared by these methods have their 5' end nucleotide sequences deleted, and thus these methods rarely produce full-length cDNA, a complete DNA copy of mRNA. This is because the reverse transcriptase used to prepare cDNA from mRNA does not necessarily have high efficiency in producing full-length cDNA. Therefore it is necessary to improve these prior art methods in order to efficiently carry out the above expression cloning.

In addition, in order to carry out the functional analysis of genes, it is essential to clone full-length cDNA sequences and express proteins from them. Therefore, it has been necessary to construct cDNA libraries containing enriched full-length cDNA for efficient expression cloning.

The present inventors have intensively studied to solve the above problems. As a result, the present inventors have succeeded in constructing a full-length cDNA library by using the oligo-capping method; establishing an assay system using 293EBNA cells; and isolating a new DNA (cDNA) encoding a protein having a function of activating NF- κ B by using the assay system. This new DNA molecule induced NF- κ B activation by its expression in 293EBNA cells. This result shows that this new DNA is a signal transduction molecule involved in NF- κ B activation. Thus, the present invention has been completed.

That is, the present invention relates to:

- (1) A purified and isolated protein selected from the group consisting of:
- (a) a protein that activates NF- κ B which consists of an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178; and
- (b) a protein that activates NF- κ B and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, or 178.
- (2) A purified and isolated protein that activates NF- κ B and comprises an amino acid sequence having at least 95% identity to the protein according to above item (1) over the entire length thereof.
- (3) An isolated polynucleotide which comprises a nucleotide sequence encoding a protein selected from the group consisting of:
- (a) a protein which comprises an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178; and
- (b) a protein that activates NF- κ B and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence represented by SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93,

95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178.

(4) An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide represented by SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177; and a polynucleotide sequence complementary to said polynucleotide sequence;

(b) a polynucleotide sequence encoding a protein that activates NF- κ B and hybridizing with a polynucleotide having the polynucleotide sequence of (a) under stringent conditions; and

(c) a polynucleotide sequence which encodes a protein that activates NF- κ B and consists of a polynucleotide sequence having at least one nucleotide deletion, substitution or addition in a polynucleotide sequence represented by SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177.

(5) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to above item (3) over the entire length thereof.

(6) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that activates NF- κ B and has at least 95% identity to the polynucleotide sequence according to above item (4) over the entire length thereof.

(7) A purified and isolated protein encoded by the polynucleotide according to any one of above items (3) to (6).

- (8) A recombinant vector which comprises a polynucleotide according to any one of above items (3) to (6).
- (9) A transformed cell which comprises the recombinant vector according to above item (8).
- (10) A membrane of the cell according to above item (9), when the protein according to above item (1) or (2) is a membrane protein.
- (11) A process for producing a protein comprising,
- (a) culturing a transformed cell comprising the isolated polynucleotide according to any one of items (3) to (6) under conditions providing expression of the encoded protein; and
 - (b) recovering the protein from the culture.
- (12) A process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the protein according to above item (1), (2) or (7) in a subject comprising:
- (a) determining the presence or absence of a mutation in the nucleotide sequence encoding said protein in the genome of said subject; and/or
 - (b) analyzing the amount of expression of said protein in a sample derived from said subject,
- wherein a diagnosis of disease is made when the amount of the protein expressed is 2-fold or higher than normal, or half or lower than normal.
- (13) A method for screening a compound in respect of activity to inhibit or promote NF- κ B activation, which comprises the steps of:
- (a) providing a cell with a gene encoding a protein that activates NF- κ B, and a component that provides a detectable signal associated with activation of NF- κ B;
 - (b) culturing a transformed cell under conditions, which permit the expression of the gene in the transformed cell;
 - (c) contacting the transformed cell with one or more compounds;
 - (d) measuring the detectable signal; and
 - (e) isolating or identifying as an activator compound a compound that increases said detectable signal 2-fold or higher than normal and/or isolating or identifying as an inhibitor

compound a compound that decreases said detectable signal half or less than normal.

(14) A process for producing a pharmaceutical composition, which comprises the steps of:

(a) providing a cell with a gene encoding a protein that activates NF- κ B, and a component capable of providing a detectable signal;

(b) culturing a transformed cell under conditions, which permit the expression of the gene in the transformed cell;

(c) contacting the transformed cell with one or more candidate compounds;

(d) measuring the detectable signal;

(e) isolating or identifying as an activator compound a compound that increases said detectable signal 2-fold or higher than normal and/or isolating or identifying as an inhibitor compound a compound that decreases said detectable signal half or less than normal; and

(f) optimizing the isolated or identified compound as a pharmaceutical composition.

(15) A kit for screening a compound in respect of activity to inhibit or promote NF- κ B activation, which comprises:

(a) a cell comprising a gene encoding a protein that activates NF- κ B, and a component that provides a detectable signal upon activation of NF- κ B; and

(b) reagents for measuring the detectable signal.

(16) A monoclonal or polyclonal antibody that specifically binds to the protein according to above item (1), (2) or (7).

(17) A process for producing a monoclonal or polyclonal antibody according to above item that specifically binds to the protein of above item (1),(2) or (7), which comprises administering the protein according to above item (1), (2) or (7) as an antigen or epitope-bearing fragments to a non-human animal.

(18) An antisense oligonucleotide complementary to the polynucleotide according to any one of above items (3) to (6), which prevents NF- κ B activator protein expression.

(19) A ribozyme which inhibits NF- κ B activation by cleavage of RNA that encodes the protein of above item (1), (2) or (7), or by cleavage of RNA that encodes some protein of the pathway that leads to I κ B degradation.

- (20) A method for treating a disease, which comprises administering to a subject an amount of a compound screened by the process according to above item (13), and/or a monoclonal or polyclonal antibody according to above item (16), and/or an antisense oligonucleotide according to above item (18), and/or a ribozyme according to above item (19) effective to treat a disease selected from the group consisting of inflammation, autoimmune diseases, infectious disease and cancers.
- (21) A pharmaceutical composition produced according to the process of item (14) as an inhibitor or promoter of NF- κ B activation.
- (22) A pharmaceutical composition according to item (21) for the treatment of inflammation, autoimmune diseases, cancers and viral infections.
- (23) A method of treating inflammation, autoimmune diseases, cancers and viral infections, which comprises administering a pharmaceutical composition produced according to the process of above item (14) to a patient suffering from NF- κ B activation.
- (24) A pharmaceutical composition according to item (21) for the treatment of GVHD, dermatosis such as toxic epidermal necrolysis, proliferative nephritides such as IgA nephritis, purpuric nephritis and lupus nephritis, and fulminant hepatitis.
- (25) A method of treating GVHD, dermatosis such as toxic epidermal necrolysis, proliferative nephritides such as IgA nephritis, purpuric nephritis and lupus nephritis, and fulminant hepatitis, which comprises administering a pharmaceutical composition produced according to the process of above item (14) to a patient suffering from inhibition of NF- κ B.
- (26) A pharmaceutical composition which comprises a monoclonal or polyclonal antibody according to item (16) as an active ingredient.
- (27) A pharmaceutical composition which comprises an antisense oligonucleotide according to item (18) as an active ingredient.
- (28) The pharmaceutical composition according to item (26) or (27), wherein the target disease is selected from the group consisting of inflammation, autoimmune diseases, infectious diseases and cancers.
- (29) A method for obtaining a novel gene having a function,

which comprises at least the following steps:

- (a) constructing a full-length cDNA library by the oligo-capping method;
- (b) cotransfecting the full-length cDNA and a plasmid containing a factor emitting a signal indicative of the presence of a protein having the function into cells; and
- (c) selecting a plasmid emitting the signal.

(30) A computer-readable medium on which a sequence data set has

been stored, said sequence data set comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178.

(31) A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to above item (30) with data of said other nucleotide sequences and/or amino acid sequences.

(32) An insoluble substrate to which polynucleotide comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88 and 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177, are fixed.

(33) An insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15,

17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178, are fixed.

At first, in order to further clarify the basic feature of the present invention, the present invention is explained by following how the present invention is completed. In order to obtain a new gene having a function of activating NF- κ B, the following experiments were carried out as shown in the examples. First, using the oligo-capping method, a full-length cDNA was produced from mRNA prepared from normal human lung fibroblasts (purchased from Sanko Junyaku Co., Ltd.), and a full-length cDNA library was constructed in which the cDNA was inserted into the vector pME18S-FL3 (GenBank Accession AB009864). Next, the cDNA library was introduced into E. coli cells, and plasmid preparation was carried out per clone. Then, the pNK κ B-Luc reporter plasmid (STRATAGENE) containing a DNA encoding luciferase under control of a promoter activated by NF- κ B and the above full-length cDNA plasmid were cotransfected into 293-EBNA cells (Invitrogen). After 24 or 48 hours of culture, luciferase activity was measured, and the plasmid with significantly increased luciferase activity compared to that of a control experiment (vector pME18S-FL3 is introduced into a cell in place of a full-length cDNA) was selected (the selected plasmid showed a 10-fold or more increase in luciferase activity compared to that of the control experiment), and the entire nucleotide sequence of the cDNA cloned into the plasmid was determined. The protein encoded by the cDNA thus obtained shows that this protein is a signal transduction molecule involved in NF- κ B activation.

The present invention is described in detail below.

Related to the amino acid sequences of SEQ ID NOs. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147,

149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178, the present invention provides for a protein that:

- (a) comprises one of the above amino acid sequences;
- (b) is a peptide having one of the above amino acid sequences;
- (c) activates NF- κ B and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in the above amino acid sequences;
- (d) comprises an amino acid sequence, which has at least 95% identity, preferably at least 97-99% identity, to an amino acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178, over the entire length thereof.

"Identity" as known in the art, is a relationship between two or more protein sequence or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between protein or polynucleotide sequences, as determined by the match between protein or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods. Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. "Identity" can be determined by using the BLAST program (for example, Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215: p403-410 (1990), Altschul SF, Madden TL, Schaffer AA, Zhang Z, Miller W, Lipman DJ., Nucleic Acids Res. 25: p3389-3402 (1997))

The Examples described below demonstrate that the protein consisting of an amino acid sequence of the above SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121,

123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178, is capable of activating NF- κ B.

Related to the polynucleotide sequences of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177, the present invention further provides an isolated polynucleotide that:

(a) comprises a nucleotide sequence, which has at least 95% identity, preferably at least 97-99% identity to one of the above sequences;

(b) is a polynucleotide of one of the above sequences; or

(c) has a nucleotide sequence encoding a protein which has at least 95% identity, preferably, at least 97-99% identity, to the amino acid sequence of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178.

Polynucleotides which are identical or almost identical to nucleotide sequences contained in the above nucleotide sequences may be used as hybridization probes to isolate full-length cDNA and genomic clones encoding the protein of the present invention, or cDNA or genomic clones of other genes that have a high sequence similarity to the above sequences, or genomic clones, or may be used as primers for nucleic acid amplification reactions. Typically, these nucleotide sequences are 70% identical, preferably 80% identical, more preferably 90% identical, most preferably 95% identical to the above sequences. The probes or primers will generally comprises at least 15 nucleotides, preferably 30 nucleotides and may have 50 nucleotides. Particularly preferred probes will have between 30 and 50 nucleotides. Particularly preferred primers have between 20 and 25 nucleotides.

The polynucleotide of the present invention may be either in the form of a DNA such as cDNA, a genomic DNA obtained by cloning or synthetically produced, or may be in

the form of RNA such as mRNA. The polynucleotide may be single-stranded or double-stranded. The double-stranded polynucleotides may be double-stranded DNA, double-stranded RNA or DNA:RNA hybrid. The single-stranded polynucleotide may be sense strand also known as coding strand or antisense strand also known as non-coding strand.

Those skilled in the art can prepare a protein having the same NF- κ B activating activity as the protein having an amino acid sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178, by means of appropriate substitution of an amino acid in the protein using known methods. One such method involves using conventional mutagenesis procedures for the DNA encoding the protein. Another method is, for example, site-directed mutagenesis (e.g., Mutan-Super Express Km Kit from Takara Shuzo Co., Ltd.). Mutations of amino acids in proteins may also occur in nature. Thus, the present invention also includes a mutated protein which is capable of activating NF- κ B and which has at least one amino acid deletion, substitution or addition relative to the protein of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178, and the DNA encoding the protein. The number of mutations is preferably up to 10, more preferably up to 5, most preferably up to 3.

The substitutions of amino acids are preferably conservative substitutions, specific examples of which are substitutions within the following groups: (glycine, alanine), (valine, isoleucine, leucine), (aspartic acid, glutamic acid), (asparagine, glutamine), (serine, threonine), (lysine, arginine) and (phenylalanine, tyrosine).

Based on the nucleotide sequences (e.g., SEQ ID NO: 2) encoding a protein

consisting of an amino acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178, or a fragment thereof, those skilled in the art can routinely isolate a DNA with a high sequence similarity to these nucleotide sequences by using hybridization techniques and the like, and obtain proteins having the same NF- κ B activating activity as the protein having of an amino acid sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178. Thus, the present invention also includes a protein that activates NF- κ B and comprises an amino acid sequence having a high identity to the amino acid sequence of the above SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178. "High identity" refers to an amino acid sequence having an identity of at least 90%, preferably at least 97-99% over the entire length of an amino acid sequence expressed by the above SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 or 178.

The proteins of the present invention may be natural proteins derived from any human or animal cells or tissues, chemically synthesized proteins, or proteins obtained by genetic recombination techniques. The protein may or may not be subjected to post-translational modifications such as sugar chain addition or phosphorylation.

The present invention also includes a polynucleotide encoding the above protein of the present invention. Examples of nucleotide sequences encoding a protein consisting of an amino acid sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178 include nucleotide sequences of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177. The DNA includes cDNA, genomic DNA, and chemically synthesized DNA. In accordance with the degeneracy of the genetic code, at least one nucleotide in the nucleotide sequence encoding a protein consisting of an amino acid sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178 can be substituted with other nucleotides without altering the amino acid sequence of the protein produced from the gene. Therefore, the DNA sequences of the present invention also include nucleotide sequences altered by substitution based on the degeneracy of the genetic code. Such DNA sequences can be synthesized using known methods.

The DNA of the present invention includes a DNA which encodes a protein capable of activating NF- κ B and hybridizes under stringent conditions with the DNA sequence of the above nucleotide sequence of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150,

151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177. Stringent conditions are apparent to those skilled in the art, and can be easily attained in accordance with various laboratory manuals such as T. Maniatis et al., *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Laboratory 1982, 1989.

That is, "stringent conditions" refer to overnight incubation at 37°C in a hybridization solution containing 30% formamide, 5 x SSC (0.75 M NaCl, 75mM trisodium citrate), 5 x Denhardt's solution, 0.5% SDS, 100 μ g/ml denatured, sheared salmon sperm DNA) followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 37°C (low stringency). Preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 40% formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 42°C (moderate stringency). More preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 50% formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 50°C (high stringency). The DNA sequence thus obtained must encode a protein capable of activating NF- κ B.

The present invention also includes a polynucleotide comprising a nucleotide sequence which encodes a protein capable of activating NF- κ B and has a high sequence similarity to the nucleotide sequence of the polynucleotide according to above item (3) or (4). Typically these nucleotide sequence are 95% identical, preferably 97% identical, more preferably 98-99% identical, most preferably at least 99% identical to the nucleotide sequence of the polynucleotide according to above item (3) or (4) over the entire length thereof.

The above nucleotide sequence of the present invention can be used to produce the above protein using recombinant DNA techniques. In general, the DNA and peptide of the present invention can be obtained by:

(A) cloning the DNA encoding the protein of the present invention;

- (B) inserting the DNA encoding the entire coding region of the protein or a part thereof into an expression vector to construct a recombinant vector;
- (C) transforming host cells with the recombinant vector thus constructed; and
- (D) culturing the obtained cells to express the protein or its analogue, and then purifying it by column chromatography.

General procedures necessary to handle DNA and recombinant host cells (e.g., *E. coli*) in the above steps are well known to those skilled in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. All the enzymes, reagents, etc., used in these procedures are commercially available, and unless otherwise stated, such commercially available products can be used according to the use conditions specified by the manufacturer's instructions to attain completely its objects. The above steps (A) to (D) can be further illustrated in more details as follows.

Techniques for cloning the DNA encoding the protein of the present invention include, in addition to the methods described in the specification of the present application, PCR amplification using a synthetic DNA having a part of the nucleotide sequence of the present invention (e.g., SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177) as a primer, and selection of the DNA inserted into a suitable vector by hybridization with a labeled DNA fragment encoding a partial or full coding region of the protein of the present invention or a labeled synthetic DNA. Another technique involves direct amplification from total RNAs or mRNA fractions prepared from cells or tissues, using the reverse transcriptase polymerase chain reaction (RT-PCR method). As a DNA inserted into a suitable vector, for example, a commercially available library (e.g., from CLONTECH and STRATAGENE) can be used. Techniques for hybridization are normally used in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. Depending on the intended purpose, the cloned DNA encoding the protein of the present invention can

be used as such or if desired after digestion with a restriction enzyme or addition of a linker. The DNA thus obtained may have a nucleotide sequence of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177, or a polynucleotide of above items (3) to (6). The DNA sequence to be inserted into an expression vector in the above step (B) may be a full-length cDNA or a DNA fragment encoding the above full-length protein, or a DNA fragment constructed so that it expresses a part thereof.

Thus, the present invention also includes a recombinant vector, which comprises the above DNA sequence. The expression vector for the protein of the present invention can be produced, for example, by excising the desired DNA fragment from the DNA encoding the protein of the present invention, and ligating the DNA fragment downstream of a promoter in a suitable expression vector.

Expression vectors for use in the present invention may be any vectors derived from prokaryotes (e.g., *E. coli*), yeast, fungi, insect viruses and vertebrate viruses so long as such vectors are replicable. However, the vectors should be selected to be compatible with microorganisms or cells used as hosts. Suitable combinations of host cell – expression vector systems are selected depending on the desired expression product.

When microorganisms are used as hosts, plasmid vectors compatible with these microorganisms are generally used as replicable expression vectors for recombinant DNA molecules.

For example, the plasmids pBR322 and pBR327 can be used to transform *E. coli*. Plasmid vectors normally contain an origin of replication, a promoter, and a marker gene conferring upon a recombinant DNA a phenotype useful for selecting the cells transformed with the recombinant DNA. Example of such promoters include a β -lactamase promoter, lactose promoter and tryptophan promoter. Examples of such marker genes include an ampicillin resistance gene, and a tetracycline resistance gene. Examples of suitable

expression vectors include the plasmids pUC18 and pUC19 in addition to pBR322, pBR327.

In order to express the DNA of the present invention in yeast, for example, YEp24 can be used as a replicable vector. The plasmid YEp24 contains the URA3 gene, which can be employed as a marker gene. Examples of promoters in expression vectors for yeast cells include promoters derived from genes for 3-phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase and alcohol dehydrogenase.

Examples of promoters and terminators for use in expression vectors to express the DNA of the present invention in fungal cells include promoters and terminators derived from genes for phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dehydrogenase (GAPD) and actin. Examples of suitable expression vectors include the plasmids pPGACY2 and pBSFAHY83.

Examples of promoters for use in expression vectors to express the DNA of the present invention in insect cells include a polyhedrin promoter and P10 promoter.

Recombinant vectors used to express the DNA of the present invention in animal cells normally contain functional sequences to regulate genes, such as an origin of replication, a promoter to be placed upstream of the DNA of the present invention, a ribosome-binding site, a polyadenylation site and a transcription termination sequence. Such functional sequences, which can be used to express the DNA of the present invention in eukaryotic cells, can be obtained from viruses and viral substances. Examples of such functional sequences include an SR α promoter, SV40 promoter, LTR promoter, CMV (cytomegalovirus) promoter and HSV-TK promoter. Among them, a CMV promoter and SR α promoter can be preferably used. As promoters to be placed inherently upstream of the gene encoding the protein of the present invention, any promoters can be used so long as they are suitable for use in the above host-vector systems. Examples of origins of replication include foreign origins of replication, for example, those derived from viruses such as adenovirus, polyoma virus and SV40 virus. When vectors capable of integration into host chromosomes are used as expression vectors, origins of replication of the host chromosomes may be employed. Examples of suitable expression vectors include the

plasmids pSV-dhfr (ATCC 37146), pBPV-1(9-1) (ATCC 37111), pcDNA3.1 (INVITROGEN) and pME18S-FL3.

The present invention also includes a transformed cell, which comprises the above recombinant vector.

Microorganisms or cells transformed with the replicable recombinant vector of the present invention can be selected from remaining untransformed parent cells based on at least one phenotype conferred by the recombinant vector. Phenotypes can be conferred by inserting at least one marker gene into the recombinant vector. Marker genes naturally contained in replicable vectors can be employed. Examples of marker genes include drug resistance genes such as neomycin resistance genes, and genes encoding dihydrofolate reductase.

As hosts for use in the above step (C), any of prokaryotes (e.g., *E. coli*), microorganisms (e.g., yeast and fungi) as well as insect and animal cells can be used so long as such hosts are compatible with the expression vectors used. Examples of such microorganisms include *Escherichia coli* strains such as *E. coli* K12 strain 294 (ATCC 31446), *E. coli* X1776 (ATCC 31537), *E. coli* C600, *E. coli* JM109 and *E. coli* B strain; bacterial strains belonging to the genus *Bacillus* such as *Bacillus subtilis*; intestinal bacteria other than *E. coli*, such as *Salmonella typhimurium* or *Serratia marcescens*; and various strains belonging to the genus *Pseudomonas*. Examples of such yeast include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, and *Pichia pastoris*. Examples of such fungi include *Aspergillus nidulans*, and *Acremonium chrysogenum* (ATCC 11550).

As insect cells, for example, *Spodoptera frugiperda* (Sf cells), High FiveTM cells derived from eggs of *Trichoplusia*, etc., can be used when the virus is AcNPV. Examples of such animal cells include HEK 293 cells, COS-1 cells, COS-7 cells, HeLa cells, and Chinese hamster ovary (CHO) cells. Among them, CHO cells and HEK 293 cells are preferred.

When cells are used as hosts, combinations of expression vectors and host cells to be used vary with experimental objects. According to such combinations, two types of expression (i.e. transient expression and constitutive expression) can be included.

"Transformation" of microorganisms and cells in the above step (C) refers to introducing DNA into microorganisms or cells by forcible methods or phagocytosis of cells and then transiently or constitutively expressing the trait of the DNA in a plasmid or an intra-chromosome integrated form. Those skilled in the art can carry out transformation by known methods [see e.g., "Idenshi Kougaku Handbook (Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.]. For example, in the case of animal cells, DNA can be introduced into cells by known methods such as DEAE-dextran method, calcium-phosphate-mediated transfection, electroporation, lipofection, etc. For stable expression of the protein of the present invention using animal cells, there is a method in which selection can be carried out by clonal selection of the animal cells containing the chromosomes into which the introduced expression vectors have been integrated. For example, transformants can be selected using the above selectable marker as an indication of successful transformation. In addition, the animal cells thus obtained using the selectable marker can be subjected to repeated clonal selection to obtain stable animal cell strains highly capable of expressing the protein of the present invention. When a dihydrofolate reductase (DHFR) gene is used as a selectable marker, one can culture animal cells while gradually increasing the concentration of methotrexate (MTX) and select the resistant strains, thereby amplifying the DNA encoding the protein of the present invention together with the DHFR gene to obtain animal cell strains having higher levels of expression.

The above transformed cells can be cultured under conditions which permit the expression of the DNA encoding the protein of the present invention to produce and accumulate the protein of the present invention. In this manner, the protein of the present invention can be produced. Thus, the present invention also includes a process for producing a protein, which comprises culturing a transformed cell comprising the isolated polynucleotide according to above item (3) to (6) under conditions providing expression of the encoded protein and recovering the protein from the culture.

The above transformed cells can be cultured by methods known to those skilled in the art (see e.g., "Bio Manual Series 4", YODOSHA CO., LTD.). For example, animal

cells can be cultured by various known animal cell culture methods including attachment culture such as Petri dish culture, multitray type culture and module culture, attachment culture in which cells are attached to cell culture carriers (microcarriers), suspension culture in which productive cells themselves are suspended. Examples of media for use in the culture include media commonly used for animal cell culture, such as D-MEM and RPMI 1640.

In order to separate and purify the protein of the present invention from the above culture, suitable combinations of per se known separation and purification methods can be used. Examples such methods include methods based on solubility, such as salting-out and solvent precipitation; methods based on the difference in charges, such as ion-exchange chromatography; methods mainly based on the difference in molecular weights, such as dialysis, ultrafiltration, gel filtration and SDS-polyacrylamide gel electrophoresis; methods based on specific affinity, such as affinity chromatography; methods based on the difference in hydrophobicity, such as reverse phase high performance liquid chromatography; and methods based on the difference in isoelectric points, such as isoelectric focusing. For example, a protein of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxyapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation or purification.

The protein of the present invention can also be produced as a fusion protein with another protein. These fusion proteins are also included within the present invention. For the expression of such fusion proteins, any vectors can be used so long as the DNA encoding the protein can be inserted into the vectors and the vectors can express the fusion protein. Examples of proteins to which a polypeptide of the present invention can be fused include glutathione S-transferase (GST) and a hexa-histidine sequence (6 x His). The

fusion protein of the protein of the present invention with another protein can be advantageously purified by affinity chromatography using a substance with an affinity for the fusion partner protein. For example, fusion proteins with GST can be purified by affinity chromatography using glutathione as a ligand.

The present invention also includes an inhibitory protein, i.e., a protein capable of inhibiting the activity of the protein of above item (7). Examples of such inhibitory proteins include antibodies, or other proteins that bind to active sites of a protein of the above item (7), thereby inhibiting the expression of their activity.

The present invention also relates to an antibody that specifically binds the protein of the present invention or a fragment thereof, and to production of such an antibody. The antibody is not specifically limited so long as it can recognize the protein of the present invention. Examples of such antibodies include polyclonal antibodies, monoclonal antibodies and their fragments, single chain antibodies and humanized antibodies. Antibody fragments can be produced by known techniques. Examples of such antibody fragments include, but not limited to, $F(ab')_2$ fragments, Fab' fragments, Fab fragments and Fv fragments. The antibody that specifically binds the protein of the present invention can be produced using the protein of the present invention or a peptide thereof as an immunogen according to per se known process for producing antibodies or antisera. For example, a monoclonal or polyclonal antibody can be produced by administering the protein according to above item (1) or (2) as an antigen or epitope-bearing fragments to a non-human animal. Such methods are described, for example, in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition, an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

In the case of polyclonal antibodies, for example, the protein of the present invention or a peptide thereof can be injected to animals such as rabbits to produce antibodies directed against the protein or peptide, and then their blood can be collected. The polyclonal antibodies can be purified from the blood, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

In the case of monoclonal antibodies, for example, animals such as mice are immunized with the protein of the present invention, their spleen is removed and homogenized to obtain spleen cells, which are then fused with mouse myeloma cells by using a reagent such as polyethylene glycol. From the resulting hybrid cells (i.e. hybridoma cells), the clone producing the antibody directed against the protein of the present invention can be selected. Then, the resulting clonal hybridoma cells can be implanted intraperitoneally into mice, the ascitic fluid recovered from the mice. The resulting monoclonal antibody can be purified, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

When the resulting antibody is used to administer it to humans, it is preferably used as a humanized antibody or human antibody in order to reduce its immunogenicity. The humanized antibody can be produced using transgenic mice or other mammals. For a general review of these humanized antibodies and human antibodies, see, for example, Morrison, S.L. et al., *Proc. Natl. Acad. Sci. USA*, 81:6851-6855 (1984); Jones, P.T. et al., *Nature* 321:522-525 (1986); Hiroshi Noguchi, *Igaku no Ayumi (J. Clin. Exp. Med.)* 167:457-462 (1993); Takashi Matsumoto, *Kagaku to Seibutsu (Chemistry and Biology)* 36:448-456 (1998). Humanized chimeric antibodies can be produced by linking a V region of a mouse antibody to a C region of a human antibody. Humanized antibodies can be produced by substituting a sequence derived from a human antibody for a region other than a complementarity-determining region from a mouse monoclonal antibody. In addition, human antibodies can be directly produced in the same manner as the production of conventional monoclonal antibodies by immunizing the mice whose immune systems have been replaced with human immune systems. These antibodies can be used to isolate or to identify clones expressing the protein or to purify the protein of the present invention from a cell extract or transformed cells producing the protein of the present invention. These proteins can also be used to construct ELISA, RIA (radioimmunoassay) and western blotting systems. These assay systems can be used for diagnostic purposes for detecting an amount of the protein of the present invention present in a body sample in a tissue or a fluid

in the blood of an animal, preferably human. For example, they can be used for diagnosis of a disease characterized by undesirable activation of HF- κ B resulting from (expression) abnormality of the protein of the present invention, such as inflammation, autoimmune disease, infection (for example, HIV infection), cancer and the like. In order to provide a basis for diagnosis of a disease, a standard value must be established. However, this is a well-known technique to those skilled in the art. For example, a method of calculating the standard value comprises binding a body fluid or a cell extract of normal individual of a human or an animal to an antibody against the protein of the present invention under a suitable condition for the complex formation, detecting the amount of the antibody-protein complex by chemical or physical means and then calculating the standard value for the normal sample using a standard curve prepared from a standard solution containing a known amount of an antigen (the protein of the present invention). The presence of a disease can be confirmed by deviation from the standard value obtained by comparison of the standard value with the value obtained from a sample of an individual latently suffering from a disease associated with the protein of the present invention. These antibodies can also be used as reagents for studying functions of the protein of the present invention.

The antibodies of the present invention can be purified and then administered to patients characterized by undesirable activation of HF- κ B resulting from (expression) abnormality of the protein of the present invention, such as inflammation, autoimmune disease, infection (such as HIV infection), cancer and the like. Thus in another aspect, the present invention is a pharmaceutical composition which comprises the above antibody as an active ingredient, and therapy using the antibody of the present invention. In such pharmaceutical compositions, the active ingredient may be combined with other therapeutically active ingredients or inactive ingredients (e.g., conventional pharmaceutically acceptable carriers or diluents such as immunogenic adjuvants) and physiologically non-toxic stabilizers and excipients. The resulting combinations can be sterilized by filtration, and formulated into vials after lyophilization or into various dosage forms in stabilized and preservable aqueous preparations. Administration to a patient can be

intra-arterial administration, intravenous administration and subcutaneous administration, which are well known to those skilled in the art. The dosage range depends upon the weight and age of the patient, route of administration and the like. Suitable dosages can be determined by those skilled in the art. These antibodies exhibit therapeutic activity by inhibiting the NF- κ B activation mediated by the protein of the present invention.

The DNA of the present invention can also be used to isolate, identify and clone other proteins involved in intracellular signal transduction processes. For example, the DNA sequence encoding the protein of the present invention can be used as a "bait" in yeast two-hybrid systems (see e.g., Nature 340:245-246 (1989)) to isolate and clone the sequence encoding a protein ("prey") which can associate with the protein of the present invention. In a similar manner, it can be determined whether the protein of the present invention can associate with other cellular proteins (e.g., NIK and TRAF2). In another method, proteins which can associate with the protein of the present invention can be isolated from cell extracts by immunoprecipitation [see e.g., "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] using antibodies directed against the protein of the present invention. In still another method, the protein of the present invention can be expressed as a fusion protein with another protein as described above, and immunoprecipitated with an antibody directed against the fusion protein in order to isolate a protein which can associate with the protein of the present invention.

The diagnostic assays offer a process for diagnosing diseases or determining a susceptibility to the diseases through detection of mutation in a gene for a protein according to item (1), (2) or (7) which has a function of activating NF- κ B, by the methods described. In addition, such diseases may be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of protein or mRNA. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, for example, nucleic acid amplification methods such as RT-PCR, and methods such as RNase protection assay, Northern blotting and other hybridization methods. Assay techniques that can be used

to determine levels of a protein in a sample derived from a host are well-known to those skilled in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western blot analysis and ELISA assays. The DNA of the present invention can be used to detect abnormality in the DNA or mRNA encoding the protein of the present invention or a peptide fragment thereof. The invention relates to a method for diagnosing a disease, or susceptibility to a disease associated with the expression of the protein according to above item (1), (2) or (7) in a subject, which comprises determining mutations in the polynucleotide sequence encoding the protein. Thus, for example, the DNA of the present invention is useful for gene diagnosis regarding damage, mutations, and reduced, increased or over- expression of the DNA or mRNA. That is, the present invention includes a method for diagnosing a disease associated with the expression or activity of NF- κ B in a subject, which comprises the steps of:

A process for diagnosing a disease or susceptibility to a disease in a subject related to expression or activity of the protein of above item (1) or (2) in a subject comprising:

- (a) determining the presence or absence of a mutation in the nucleotide sequence encoding said protein in the genome of said subject, and/or
- (b) analyzing the amount of expression of said protein in a sample derived from said subject,

wherein a diagnosis of disease is made when the amount of the protein expressed is 2-fold or higher than normal, or half or lower than normal.

When the nucleotide sequence encoding the protein of above item (1), (2) or (7) which has a function of activating NF- κ B, contains a mutation according to the above step (a), the mutation may cause a disease associated with NF- κ B activation. When the amount of the expression of the protein of above item (1), (2) or (7) is different from the normal value according to the above step (b), the abnormal expression of the novel protein of the present invention which acts to activate NF- κ B may be responsible for diseases associated with NF- κ B activation. In the above step (a), determination of the presence or absence of a mutation in the nucleotide sequence encoding the protein of above item (1),(2) or (7) which has a function of activating NF- κ B, may involve RT-PCR using a part of the

nucleotide sequences of genes encoding these proteins as a primer, followed by conventional DNA sequencing to detect the presence or absence of the mutation. PCR-SSCP [Genomics 5:874-879 (1989); "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] can also be used to determine the presence or absence of the mutation.

Measurement of the amount of the expression of the protein in the above step (b) may involve, for example, using the antibody of above item (16). Sequencing the nucleotide sequence may involve, for example, RT-PCR using a part of the nucleotide sequence of the gene of above items (3) to (6) as a primer, followed by conventional DNA sequencing to detect the presence or absence of the mutation. PCR-SSCP [Genomics 5:874-879 (1989); "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] can also be used to determine the presence or absence of the mutation.

The present invention also relates to a method for screening compounds which inhibit or promote NF- κ B activation using the proteins of the invention, which comprises the steps of:

- (a) providing a cell with a gene encoding a protein that activates NF- κ B, and a component that provides a detectable signal upon activation of NF- κ B;
- (b) culturing the transformed cell under conditions, which permit the expression of the gene in the transformed cell;
- (c) contacting the transformed cell with one or more compounds; and
- (d) measuring the detectable signal; and
- (e) isolating or identifying as an activator compound a compound that increases said detectable signal 2-fold or higher than normal and isolating or identifying as an inhibitor compound a compound that decreases said detectable signal half or higher than normal.

Examples of components capable of providing a detectable signal include reporter genes. Reporter genes are used instead of directly detecting the activation of transcription factors of interest. The transcriptional activity of a promoter of a gene is analyzed by

linking the promoter to a reporter gene and measuring the activity of the product of the reporter gene ("Bio Manual Series 4" (1994), YODOSHA CO., LTD.).

Any peptide or protein can be used so long as those skilled in the art can measure the activity or amount of the expression product (including the amount of the produced mRNA) of the reporter genes. For example, enzymatic activity of chloramphenicol acetyltransferase, β -galactosidase, luciferase, etc., can be measured. Any reporter plasmids can be used to evaluate NF- κ B activation so long as the reporter plasmids have an NF- κ B recognition sequence inserted upstream of the reporter gene. For example, pNF- κ B-Luc (STRATAGEGE) can be used. Other examples include NF- κ B dependent reporter plasmids described in Tanaka S. et al., J. Vet. Med. Sci. Vol.59 (7); Rothe M. et al., Science Vol.269, p.1424-1427 (1995).

Any host cells may be used so long as NF- κ B activation can be detected in the host cells. Preferred host cells are mammalian cells such as 293-EBNA cells. Transformation and culture of the cells can be carried out as described above.

In a specific embodiment, the method for screening a compound which inhibits or promotes NF- κ B activation comprises culturing the transformed cell for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. The reporter activity can be measured by methods known in the art (see e.g., "Bio Manual Series 4" (1994), YODOSHA CO., LTD.). Examples of test compounds include, but not limited to, low molecular weight compounds and peptides. Test compounds may be artificially synthesized compounds or naturally occurring compounds. Test compounds may be a single compound or mixtures. Examples of such detectable signals which may be measured include the amount of mRNA or proteins for genes whose expression is known to be induced by NF- κ B activation (e.g., genes for IL-1 and TNF- α) in addition to the above reporter genes. The amount of mRNA can be measured, for example, by northern hybridization, RT-PCR, etc. The amount of proteins can be measured, for example, by using antibodies. The antibodies may be produced by known methods. Commercially available antibodies (from, e.g., Wako Pure

Chemical Industries, Ltd.) can also be used.

It is also possible to produce a pharmaceutical composition according to the following steps (a) to (f):

- (a) providing a cell with a gene encoding a protein that activates NF- κ B, and a component that provides a detectable signal upon activation of NF- κ B;
- (b) culturing the transformed cell under conditions, which permit the expression of the gene in the transformed cell;
- (c) contacting the transformed cell with one or more candidate compounds;
- (d) measuring the detectable signal;
- (e) isolating or identifying as an activator compound a compound that increases said detectable signal 2-fold or higher than normal and isolating or identifying as an inhibitor compound a compound that decreases said detectable signal half or less than normal; and
- (f) optimizing the isolated or identified compound as a pharmaceutical composition.

The protein of the present invention may also be used in a method for the structure-based design of an agonist, antagonist or inhibitor of the protein, by:

- (a) determining in the first instance the three-dimensional structure of the protein;
- (b) deducing the three-dimensional structure for the likely reactive or binding site(s) of an agonist, antagonist or inhibitor;
- (c) synthesising candidate compounds that are predicted to bind to or react with the deduced binding or reactive site; and
- (d) testing whether the candidate compounds are indeed agonists, antagonists or inhibitor.

The present invention also includes a compound obtainable by the above screening method. However, the screening method of the present invention is not limited to the above method. The present invention also includes a process for producing the pharmaceutical composition by the method of above item (14).

There is no special limitation to the above candidate compounds. Such compounds include low molecular weight compounds and peptides. They may be artificially synthesised compounds and naturally occurring compounds. As the compounds obtained by the above screening methods have a function of inhibiting or promoting NF- κ B

activation, they are useful as therapeutic or preventive pharmaceuticals for the treatment of diseases resulting from unfavorable activation or inactivation of NF- κ B. In order to isolate and purify the target compounds from the mixture, it is suitable to combine the known methods such as filtration, extraction, washings, drying, concentration, crystallization, various chromatography. When obtainment of a salt of the compounds is desired, a compound which is obtained in the form of a salt can be purified as it is. A compound which is obtained in the free form can be converted into a salt by isolating and purifying a salt obtained by dispersing or dissolving the compound into a suitable solvent and then adding a desired acid or base. When the compounds or salts thereof obtained by the method of the present invention are used as a pharmaceutical composition, they can be formulated. The above compounds or their pharmaceutically acceptable salts in an amount effective as an active ingredient, and pharmaceutically acceptable carriers can be mixed. A form of formulation suitable for the mode of administration is selected. A composition suitable for oral administration includes a solid form such as tablet, granule, capsule, pill and powder, and solution form such as solution, syrup, elixir and dispersion. A form useful for parenteral administration includes sterile solution, dispersion, emulsion and suspension. The above carriers include, for example, sugars such as gelatin, lactose and glucose, starches such as corn, wheat, rice and maize, fatty acids such as stearic acid, salts of fatty acids such as calcium stearate, magnesium stearate, talc, vegetable oil, alcohol such as stearyl alcohol and benzyl alcohol, gum, and polyalkylene glycol. Examples of such liquid carriers include generally water, saline, sugar solution of dextrose and the like, glycols such as ethylene glycol, propylene glycol and polyethylene glycol.

The present invention also includes a kit for screening compounds for activity as an inhibitor or promoter of NF- κ B activation. The kit comprises reagents and the like necessary for screening compounds for inhibiting or promoting activity for NF- κ B activation, including:

- (a) a cell comprising a gene encoding a protein that activates NF- κ B, and a component that provides a detectable signal enabling detection of NF- κ B activation after activation of NF- κ B; and

(b) reagents for measuring the detectable signal.

In another aspect, the present invention relates to a diagnostic kit which comprises:

- (a) a polynucleotide of the present invention having a nucleotide sequence expressed by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62; 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 or 177;
- (b) a nucleotide sequence complementary to that of (a);
- (c) a protein of the present invention having an amino acid sequence expressed by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, or 178, or a fragment thereof; or
- (d) an antibody to the protein of the present invention of (c).

A kit comprising at least one of (a) to (d) is useful for diagnosing a disease or susceptibility to a disease such as inflammation, autoimmune diseases, infectious diseases (e.g., HIV infection) and cancers.

Because NF- κ B is involved in a wide variety of pathological conditions such as inflammation, autoimmune diseases, cancers and viral infections, it is an attractive target for drug design and therapeutic intervention. Many experiments show that the inhibition of NF- κ B activity may have significant physiological effects [see e.g., *Ann. Rheum. Dis.* 57:738-741 (1998); *American Journal of Pathology* 152:793-803 (1998); *ARTHRITIS & RHEUMATISM* 40:226-236 (1997); *Am. J. Respir. Crit. Care Med.* 158:1585-1592 (1998); *J. Exp. Med.* 188:1739-1750 (1998); *Gut* 42:477-484 (1998); *The Journal of Immunology* 161:4572-4582 (1998); *Nature Medicine* 3:894-899 (1997)]. The finding of the new protein described herein capable of activating NF- κ B has provided a new method for inhibiting an abnormal NF- κ B function. Thus, the present invention also relates to use of

a compound which inhibits the function of the protein capable of activating NF- κ B described above, for inhibiting NF- κ B activation. The compound obtained by the above screening method, which inhibits NF- κ B activation, is useful as a medicament to treat or prevent diseases characterized by undesirable activation of NF- κ B, such as inflammation, autoimmune diseases, infectious diseases (e.g., HIV infection) and cancers. Recently, it has also become apparent that NF- κ B activation inhibits apoptosis of cells. The compound obtained by the above screening method, which inhibits NF- κ B activation, may be capable of stimulating apoptosis. Diseases which may be treated by the induction of apoptosis include tumors.

On the other hand, diseases which may be treated by the inhibition of apoptosis include GVHD, skin diseases such as toxic epidermal necrolysis (TEN), proliferative nephritides (e.g., IgA nephritis, purpuric nephritis and lupus nephritis) and fulminant hepatitis. Thus, the compound obtained by the above screening method, which promotes NF- κ B activation, is useful as a medicament to treat or prevent these diseases.

In addition, the gene encoding the protein of the present invention is useful for gene therapy to treat various diseases such as cancers, autoimmune diseases, allergy diseases and inflammatory response. "Gene therapy" refers to administering into the human body a gene or a cell into which a gene has been introduced. The protein of the present invention and the DNA encoding the protein can also be used for diagnostic purposes.

The compound obtained by the screening method of the present invention or a salt thereof can be formulated into the above pharmaceutical compositions (e.g., tablets, capsules, elixirs, microcapsules, sterile solutions and suspensions) according to conventional procedures. The formulations thus obtained are safe and of low toxicity, and can be administered, for example, to humans and mammals (e.g., rats, rabbits, sheep, pigs, cattle, cats, dogs and monkeys). Administration to patients can be carried out by methods known in the art, such as intra-arterial injection, intravenous injection and subcutaneous injection. The dosage may vary with the weight and age of the patient as well as a mode of administration, but those skilled in the art can appropriately select suitable dosages. When

the compound can be encoded by DNA, the DNA can be inserted into a vector for gene therapy, and gene therapy can be carried out. The dosage and mode of administration may vary with the weight, age and symptoms of the patient, but those skilled in the art can appropriately select them. Thus, the present invention also relates to a pharmaceutical composition which comprises the above compound as an active ingredient.

In addition, the above compound is useful as a medicament to treat or prevent diseases characterized by undesirable activation of NF- κ B, such as inflammation, autoimmune diseases, viral diseases, infectious diseases and cancers. Thus, the present invention also relates to a pharmaceutical composition for inflammation, autoimmune diseases, viral diseases, cancers, etc., which comprises the above compound. Specifically, the pharmaceutical composition is useful as a therapeutic and prophylactic drug against, for example, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, diabetes, sepsis, asthma, allergic rhinitis, ischemic heart diseases, inflammatory intestinal diseases, subarachnoid hemorrhage, viral hepatitis and AIDS.

The present invention also relates to the use of a pharmaceutical composition produced according to above item (14) for manufacturing a medicament against inflammation, autoimmune diseases, viral diseases, cancers, etc. The present invention also includes an antisense oligonucleotide against a gene of any one of above items (3) to (6). An antisense oligonucleotide refers to an oligonucleotide complementary to the target gene sequence. The antisense oligonucleotide can inhibit the expression of the target gene by inhibiting RNA functions such as translation to proteins, transport to the cytoplasm and other activity necessary for overall biological functions. In this case, the antisense oligonucleotide may be RNA or DNA. The DNA sequence of the present invention can be used to produce an antisense oligonucleotide capable of hybridizing with the mRNA transcribed from the gene encoding the protein of the present invention. It is known that an antisense oligonucleotide generally has an inhibitory effect on the expression of the corresponding gene (see e.g., Saibou Kougaku Vol.13, No.4 (1994)). The oligonucleotide containing an antisense coding sequence against a gene encoding the protein of the present invention can be introduced into a cell by standard methods. The oligonucleotide

effectively blocks the translation of mRNA of the gene encoding the protein of the present invention, thereby blocking its expression and inhibiting undesirable activity.

The oligonucleotide of the present invention may be a naturally occurring oligonucleotide or its modified form [see e.g., Murakami & Makino, Saibou Kougaku Vol.13, No.4, p.259-266 (1994); Akira Murakami, Tanpakushitsu Kakusan Kouso (PROTEIN, NUCLEIC ACID AND ENZYME) Vol.40, No.10, p.1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14, No. 4 p85-95(1996)]. Thus, the oligonucleotide may have modified sugar moieties or inter-sugar moieties. Examples of such modified forms include phosphothioates and other sulfur-containing species used in the art. According to several preferred embodiments of the present invention, at least one phosphodiester bond in the oligonucleotide is substituted with the structure which can enhance the ability of the composition to permeate cellular regions where RNA with the activity to be regulated is located.

Such substitution preferably involves a phosphorothioate bond, a phosphoramidate bond, methylphosphonate bond, or a short-chain alkyl or cycloalkyl structure. The oligonucleotide may also contain at least some modified base forms. Thus, it may contain purine and pyrimidine derivatives other than naturally occurring purine and pyrimidine. Similarly, the furanosyl moieties of the nucleotide subunits can be modified so long as the essential purpose of the present invention is attained. Examples of such modifications include 2'-O-alkyl and 2'-halogen substituted nucleotides. Examples of modifications in sugar moieties at their 2-position include OH, SH, SCH₃, OCH₃, OCN or O(CH₂)_nCH₃, wherein n is 1 to about 10, and other substituents having similar properties. All the analogues are included in the scope of the present invention so long as they can hybridize with the mRNA of the gene of the present invention to inhibit functions of the mRNA.

The oligonucleotide of the present invention contains about 3 to about 50 nucleotides, preferably about 8 to about 25 nucleotides, more preferably about 12 to about 20 nucleotides. The oligonucleotide of the present invention can be produced by the well-known solid phase synthesis technique. Devices for such synthesis are commercially available from some manufactures including Applied Biosystems. Other oligonucleotides

such as phosphothioates can also be produced by methods known in the art.

The oligonucleotide of the present invention is designed to hybridize with the mRNA transcribed from the gene of the present invention. Those skilled in the art can easily design an antisense oligonucleotides based on a given gene sequence (For example, Murakami and Makino: Saibou Kougaku Vol. 13 No.4 p259-266 (1994), Akira Murakami: Tanpakushitsu Kakusan Kouso (PROTEIN, NUCLEIC ACID AND ENZYME) Vol. 40 No.10 p1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14 No. 4 p85-95 (1996)). Recent sutudy suggests that antisense oligonucleotides which are designed in a region containing 5' region of mRNA, preferably,the translation initaiation site,are most effective for the inhibition of the expression of a gene.The length of the antisense oligonucleotides is preferably 15 to 30 nucleotides and more preferably 20 to 25 nucleotides. It is important to confirm no interaction with other mRNA and no formation of secondary structure in the oligonucleotide sequence by homology search. The evaluation of whether the designed antisense oligonucleotide is functional or not can be determined by introducing the antisense oligonucleotide into a suitable cell and measuring the amount of the target mRNA, for example by northern blotting or RT-PCR, or the amount of the target protein, for example by western blotting or fluorescent antibody technique, to confirm the effect of expression inhibition

Another method includes the triple helix technique. This technique involves forming a triple helix on the targeted intra-nuclear DNA sequence, thereby regulating its gene expression, mainly at the transcription stage. The oligonucleotide is designed mainly in the gene region involved in the transcription and inhibits the transcription and the production of the protein of the present invention. Such RNA, DNA and oligonucleotide can be produced using known synthesizers.

The oligonucleotide may be introduced into the cells containing the target nucleic acid sequence by any of DNA transfection methods such as calcium phosphate method, electroporation,lipofection, microinjection, or gene transfer methods including the use of gene transfer vectors such as viruses. An antisense oligonucleotide expression vector can be prepared using a suitable retrovirus vector, then the expression vector can be introduced

into the cells containing the target nucleic acid sequence by contacting the vector with the cells in vivo or ex vivo.

The DNA of the present invention can be used in the antisense RNA/DNA technique or the triple helix technique to inhibit NF- κ B activation mediated by the protein of the present invention.

The antisense oligonucleotide against the gene encoding the protein of the present invention is useful as a medicament to treat or prevent diseases characterized by undesirable activation of NF- κ B, such as inflammation, autoimmune diseases, infectious diseases (e.g., HIV infection) and cancers. Thus, the present invention also includes a pharmaceutical composition which comprises the above antisense oligonucleotide as an active ingredient. The antisense oligonucleotide can also be used to detect such diseases using northern hybridization or PCR.

The present invention also includes a ribozyme which inhibits NF- κ B activation. A ribozyme is an RNA capable of recognizing a nucleotide sequence of a nucleic acid and cleaving the nucleic acid (see e.g., Hiroshi Yanagawa, "Jikken Igaku (Experimental Medicine) Bioscience 12: New Age of RNA). The ribozyme can be produced so that it cleaves the selected target RNA (e.g., mRNA encoding the protein of the present invention). Based on the nucleotide sequence of the DNA encoding the protein of the present invention, the ribozyme specifically cleaving the mRNA of the protein of the present invention can be designed. Such ribozyme has a complementary sequence to the mRNA for the protein of the present invention, complementarily associates with the mRNA and then cleaves the mRNA, which results in reduction or entire loss of the expression of the protein of the present invention. The level of the reduction of the expression is dependent on the level of the ribozyme expression in the target cells.

There are two types of ribozyme commonly used: a hammerhead ribozyme and a hairpin ribozyme. In particular, hammerhead ribozymes have been well studied regarding their primary and secondary structure necessary for their cleavage activity, and those skilled in the art can easily design the ribozymes nucleotided solely on the nucleotide sequence information for the DNA encoding the protein of the present invention [see e.g., Iida et al.,

Saibou Kougaku Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994)]. It is known that the hammerhead ribozymes have a structure consisting of two recognition sites (recognition site I and recognition site II forming a chain complementary to target RNA) and an active site, and cleave the target RNA at the 3'end of its sequence NUX (wherein N is A or G or C or U, and X is A or C or U) after the formation of a complementary pair with the target RNA in the recognition sites. In particular, the sequence GUC (or GUA) has been found to have the highest activity [see e.g., Koizumi, M. et al., Nucl. Acids Res. 17:7059-7071 (1989); Iida et al., Saibou Kougaku Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994); Kawasaki & Taira, Jikken Igaku (Experimental Medicine) Vol.18, No.3, p.381-386 (2000)].

Therefore the sequence GTC (or GTA) is searched out, and a ribozyme is designed to form several, up to 10 to 20 complementary base pairs around that sequence. The suitability of the designed ribozyme can be evaluated by checking whether the prepared ribozyme can cleave the target mRNA in vitro according to the method described for example in Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994). The ribozyme can be prepared by methods known in the art to synthesize RNA molecules.

Alternatively, the sequence of the ribozyme can be synthesized on a DNA synthesizer and inserted into various vectors containing a suitable RNA polymerase promoter (e.g., T7 or SP6) to enzymatically synthesize an RNA molecule in vitro. Such ribozymes can be introduced into cells by gene transfer methods such as microinjection. Another method involves inserting a ribozyme DNA into a suitable expression vector and introducing the vector into cell strains, cells or tissues. Suitable vectors can be used to introduce the ribozyme into a selected cell. Examples of vectors commonly used for such purpose include plasmid vectors and animal virus vectors (e.g., retrovirus, adenovirus, herpes or vaccinia virus vectors). Such ribozymes are capable of inhibiting the NF- κ B activation mediated by the protein of the present invention.

The present invention, moreover, relates to a process for obtaining a new gene

having a function, which comprises using the oligo-capping method to construct a full-length cDNA library, and using a signal factor indicative of the presence of a protein having the function. An example of such signal factor is a reporter gene.

Methods using a cDNA library containing a lot of non-full-length cDNAs are inefficient in obtaining many genes (cDNAs) having functions. Therefore libraries with a high ratio of the number of the full-length cDNA clones to the total number of the clones are necessary. "Full-length cDNA" refers to a complete DNA copy of mRNA from a gene. The cDNA libraries produced using the oligo-capping method contain full-length cDNA clones in a ratio of 50 to 80%, namely, a 5 to 10-fold increase in full-length cDNA clones compared to the cDNA libraries produced by prior art methods (Sumio Sugano, the monthly magazine BIO INDUSTRY Vol.16, No.11, p.19-26). Full-length cDNA clones are essential for protein expression in functional analyses of genes, and full-length cDNA clones themselves are very important materials for activity measurement. Thus, cloning of full-length cDNA is necessary for functional analyses of genes. Sequencing of the cDNA not only provides important information for establishing the primary sequence of the protein encoded by the cDNA, but also reveals the entire exon sequence. Thus, the full-length cDNA provides valuable information for identifying a gene, such as information for determining the primary sequence of a protein, exon-intron structure, the transcription initiation site of mRNA, the location of a promoter, etc.

The construction of full-length cDNA libraries by the oligo-capping method can be carried out, for example, according to the method described in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD. The reporter gene indicative of the presence of a protein having a function contains one or more suitable expression regulation sequence portion to which a protein factor such as a transcriptional factor can bind, and a structural gene portion which allows the measurement of the activation of the proteins factor. The structural gene portion may encode any peptide or protein so long as those skilled in the art can measure the activity or amount of its expression product (including the amount of the mRNA produced). For example,

chloramphenicol acetyltransferase, β -galactosidase, luciferase, etc., can be used and their enzymatic activity measured.

The oligo-capping method used herein involves substituting a cap structure with a synthetic oligo sequence by using BAP, TAP and an RNA ligase, as described in Suzuki & Sugano, "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

The process of the present invention uses an in vitro system or a cell-based system, preferably a cell-based system. Examples of such cells include cells of prokaryotes such as *E. coli*, microorganisms such as yeast and fungi, as well as insects and animals. Preferred examples include animal cells, in particular, 293-EBNA cells and NIH3T3 cells.

Examples of reporter genes indicative of the presence of a protein having a function include reporter genes containing a CREB (cAMP responsive element binding protein) binding sequence or AP-1 (activator protein-1) binding sequence at the expression regulation sequence region of the reporter genes, in addition to the NF- κ B reporter genes described herein. For example, if a gene capable of activating CREB is to be obtained, a CREB-dependent reporter plasmid and a full-length cDNA clone produced by the oligo-capping method can be cotransfected into cells, and a plasmid having increased reporter activity can be selected from the cells to attain the purpose. If a gene capable of inhibiting CREB is to be obtained, a CREB-dependent reporter plasmid and a full-length cDNA clone produced by the oligo-capping method can be cotransfected into cells, and a plasmid having decreased reporter activity can be selected from the cells to attain the purpose. These procedures may be carried out in the presence of a certain stimulus to the cells. The cDNA to be transfected into the cells may be a single clone or multiple clones which may be transfected simultaneously. One embodiment of the process of the present invention is detailed in Examples herein. Alternatively, a screening system for obtaining a gene capable of inhibiting NF- κ B activation can also be constructed by cotransfecting a full-length cDNA and a reporter gene into cells and selecting a clone having subnormally increased reporter activity.

However, the process of the present invention is not limited to these embodiments.

Because the cDNA of the present invention is full-length, its 5' end sequence is the transcription initiation site of the corresponding mRNA. Therefore the cDNA sequence can be used to identify the promoter region of the gene by comparing the cDNA with the genomic nucleotide sequence. Genomic nucleotide sequences are available from various databases when the sequences have been deposited in the databases. Alternatively, the cDNA can also be used to clone the desired sequence from a genomic library, for example, by hybridization, and determine its nucleotide sequence. Thus, by comparing the nucleotide sequence of the cDNA of the present invention with a genomic sequence, the promoter region of the gene located upstream the cDNA can be identified. In addition, the promoter fragment thus identified can be used to construct a reporter plasmid for evaluating the expression of the gene. In general, the DNA fragment spanning 2kb (preferably 1kb) upstream from the transcription initiation site can be inserted upstream of the reporter gene to produce the reporter plasmid. The reporter plasmid can be used to screen for a compound which enhances or reduces the expression of the gene. For example, such screening can be carried out by transforming a suitable cell with the reporter plasmid, culturing the transformed cell for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. These methods are also included in the scope of the present invention.

The present invention also relates to a computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59,

61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178.

In another aspect, the present invention relates to a method for calculating a homology, which comprises comparing data on the above medium with data of other nucleotide sequences. Thus, the gene and amino acid sequence of the present invention provide valuable information for determining their secondary and tertiary structure, e.g., information for identifying other sequence having a similar function and high homology. These sequences are stored on the computer-readable medium, then a database is searched using data stored in a known macromolecule structure program and a known search tool such as GCG. In this manner, a sequence in a database having a certain homology can be easily found.

The computer-readable medium may be any composition of materials used to store information or data. Examples of such media include commercially available floppy disks, tapes, chips, hard drives, compact disks and video disks. The data on the medium allows a method for calculating a homology by comparing the data with other nucleotide sequence data. This method comprises the steps of providing a first polynucleotide sequence containing the polynucleotide sequence of the present invention for the computer-readable medium, and then comparing the first polynucleotide sequence with at least one-second polynucleotide or polypeptide sequence to identify the homology.

The present invention also relates to an insoluble substrate to which polynucleotide comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177 are fixed. A plurality of the various polynucleotides which are DNA probes are fixed on a specifically processed solid substrate such as slide glass to form

a DNA microarray and then a labeled target polynucleotide is hybridized with the fixed polynucleotides to detect a signal from each of the probes. The data obtained is analyzed and the gene expression is determined.

The present invention further relates to an insoluble substrate to which polypeptides comprising all or part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178, are fixed. By mixing organism-derived cell extract with the insoluble substrate on which these proteins are fixed, it is possible to isolate or identify cell-derived components such as proteins captured on the insoluble substrate that can be expected to be useful in diagnosis or drug development.

Examples:

The following examples further illustrate, but do not limit the present invention.

Example 1: Construction of a full-length cDNA library using the oligo-capping method

(1) Preparation of RNA from human lung fibroblasts (Cryo NHLF)

Human lung fibroblasts (Cryo NHLF: purchased from Sanko Junyaku Co., Ltd.) were cultured according to the attached protocol. After repeating subculturing the cells to obtain fifty 10cm dishes containing the resulting culture, the cells were recovered with a cell scraper. Then, total RNA was obtained from the recovered cells by using the RNA extraction reagent ISOGEN (purchased from NIPPON GENE) according to the manufacturer's protocol. Then, poly A⁺ RNA was obtained from the total RNA by using an oligo-dT cellulose column according to Maniatis et al., supra.

(2) Preparation of RNA from mouse ATDC5 cells

ATDC5, a cell strain cloned from mouse EC (embryonal carcinoma) (Atsumi, T. et al.: Cell Diff. Dev., 30: p109-116)(1990) was repeatedly subcultured to obtain fifty 10cm dishes containing the resultant culture. Thereafter, poly A⁺ RNA was obtained by a method

similar to that of (1) above.

(3) Construction of a full-length cDNA library by the oligo-capping method

A full-length cDNA library was constructed from poly A⁺ RNA of the above human lung fibroblasts and ATDC5 cells by the oligo-capping method according to the method of Sugano S. et al. [e.g., Maruyama, K. & Sugano, S., *Gene*, 138:171-174 (1994); Suzuki, Y. et al., *Gene*, 200:149-156 (1997); Suzuki, Y. & Sugano, S. "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.].

(4) Preparation of plasmid DNA

The full-length cDNA library constructed as above was transfected into *E. coli* strain TOP 10 by electroporation, then spread on LB agar medium, and incubated overnight at 37°C. Then, using QIAwell 96 Ultra Plasmid Kit (QIAGEN) according to the manufacturer's protocol, the plasmids were recovered from the colonies grown on ampicillin-containing LB agar medium.

Example 2: Cloning of DNA capable of activating NF- κ B

(1) Screening of the cDNA encoding the protein capable of activating NF- κ B

293-EBNA cells (purchased from Invitrogen) were grown to 1×10^4 cells/well in a 96 well plate for cell culture for 24 hours at 37°C (in the presence of 5% CO₂) using 5% FBS containing DMEM medium. Then, 50ng of pNF κ B-Luc (purchased from STRATAGENE) and 2 μ l of the full-length cDNA prepared in above Example 1.(4) were cotransfected into the cells in a well using FuGENE 6 (purchased from Roche) according to the manufacturer's protocol. After 24 hours of culture at 37°C, the reporter activity of NF- κ B (luciferase activity) was measured using long-term luciferase assay system, PIKKA GENE LT2.0 (TOYO INK) according to the attached manufacturer's instructions. The luciferase activity was measured using Wallac ARVOTMST 1420 MULTILABEL COUNTER (Perkin Elmer).

(2) DNA sequencing

The above screening was carried out for 155,000 clones, and plasmids showing a 5-fold or more increase in luciferase activity compared to that of the control experiment

(luciferase activity of the cell into which vacant vector pME18S-FL3 is introduced instead of full-length cDNA) were selected. One pass sequencing was carried out from the 5' end of the cloned cDNA (sequencing primer: 5'-CTTCTGCTCTAAAAGCTGCG-3' (SEQ ID NO: 179)) and from the 3' end (sequencing primer: 5'-CGACCTGCAGCTCGAGCACA-3' (SEQ ID NO: 180)) so that as long sequence as possible is determined. The sequencing was carried out using the reagent Thermo Sequenase II Dye Terminator Cycle Sequencing Kit (Amersham Pharmacia Biotech) or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit (Applied Biosystems) and the device ABI PRISM 377 sequencer or ABI PRISM 3100 sequencer according to the manufacturer's instructions.

(3) Database analysis of the obtained clones

BLAST (Basic local alignment search tool) searching [S. F. Altschul et al., J. Mol. Biol., 215:403-410 (1990)] was carried out in GenBank for the obtained nucleotide sequence. The results showed that 147 clones represented 89 genes encoding new proteins capable of activating NF- κ B.

(4) Full-length sequencing

The full-length DNA sequences for the 89 new clones were determined (SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175 and 177). The amino acid sequences of the protein coding regions (open reading frames) were deduced (SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176 and 178).

Example 3: Screening compounds inhibiting NF- κ B activation

293-EBNA cells were seeded on 5% FBS containing DMEM medium in a 96-well cell culture plate to a final cell density of 1×10^4 cells/100 μ l/well, and cultured for 24

hours at 37°C in the presence of 5% CO₂. Then, 10ng of the plasmid containing the gene encoding NF- κ B activating protein of SEQ ID NO: 41 and 50ng of the reporter plasmid pNF κ B-Luc were cotransfected into the cells in a well using FuGENE 6. After 1 hour, the proteasome inhibitor MG132 (purchased from CALBIOCHEM) (Uehara T. et al., J. Biol. Chem. 274, p.15875-15882 (1999); Wang X. C. et al., Invest. Ophthalmol. Vis. Sci. 40, p.477-486) was added to the culture to a final concentration of 10 μ M. After 24 hours of culture at 37°C, the reporter activity was measured using PIKKA GENE LT2.0. The results showed that MG132 inhibited the expression of the reporter gene (Fig. 1).

EFFECTS OF THE INVENTION

As described above, the present invention provides industrially highly useful proteins capable of activating NF- κ B and genes encoding the proteins. The proteins of the present invention and the genes encoding the proteins allow not only screening for compounds useful for treating and preventing diseases associated with the excessive activation or inhibition of NF- κ B, but also production of diagnostics for such diseases. The genes of the present invention are also useful as a gene source used for gene therapy.

SEQUENCE LISTING

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          35           40           45
Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
          50           55           60
Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
          65           70           75           80
Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
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Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
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Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
              30              35              40

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              65              70              75

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 <211> 339
 <212> PRT
 <213> Homo sapiens

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 Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
 35 40 45
 Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
 50 55 60
 Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
 65 70 75 80
 Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
 85 90 95
 Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
 100 105 110
 Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
 115 120 125
 Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
 130 135 140

Lys Leu Lys Glu Ser  Tyr Lys Gln His Gly Phe Ala Ser  Ser Asp
 145 150 155 160
 Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
 165 170 175
 Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
 180 185 190
 Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
 195 200 205
 Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
 210 215 220
 Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
 225 230 235 240
 Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
 245 250 255
 Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
 260 265 270
 Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
 275 280 285
 Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
 290 295 300
 Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
 305 310 315 320
 Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
 325 330 335
 Arg Arg Arg

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 <213> Homo sapiens

<220>
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 <222> (115)..(1131)

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 Met
 1
 gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp 20 25 30	213
cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr 35 40 45	261
gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys 50 55 60 65	309
tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile 70 75 80	357
cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys 85 90 95	405
aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser 100 105 110	453
tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser 115 120 125	501
tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys 130 135 140 145	549
ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr 150 155 160	597
tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile 165 170 175	645
acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe 180 185 190	693
ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro 195 200 205	741
ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro 210 215 220 225	789
cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly 230 235 240	837

gca act tct ggt ttt c agt gct ttt aca gga caa caa ggt tat gaa	885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu	
245 250 255	
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta	933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu	
260 265 270	
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg	981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser	
275 280 285	
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg	1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg	
290 295 300 305	
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca	1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser	
310 315 320	
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg	1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg	
325 330 335	
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatTTTT	1181
Arg Arg	
catcactttc tcttttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc	1241
aaaagttcgg tgggtgttatg tccagtgtag ctttttgtat tctattattt gaggctaaaa	1301
gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg	1361
cagtttttga aagtgatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg	1421
tgatgcccta agaagcatta agaatgaagg tgttgacta atagaaacta agtacagaaa	1481
atttcagttt taggtggttg tagctgatga gttattacct catagagact gtaatattct	1541
atttggattt atattatttg atgtttgctg ttcttcaaac atttaaatca agctttggac	1601
taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg aatcattcag	1661
tgggtggagat ggccttctgg taactgaata ttaccttctg taggaaaagg tggaaaataa	1721
gcatctagaa ggttgttgtg aatgactctg tgctggcaaa aatgcttgaa acctctatat	1781
ttctttcgtt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt aataacaaaa	1841
gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca atcttaaaaa	1901
gaatcaataa aaacaaacaa ggg	1924

<210> 5
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 5

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20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
115 120 125

<210> 6

<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (605)

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cccagaaagg aggcgaggaa ggaggagtg tgtgagagga gggagcaaaa agctcacct 180
aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
Met Ala Gly Ala
1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
5 10 15 20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
40 45 50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
 Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
 55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
 Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
 70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
 Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
 85 90 95 100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572
 Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
 105 110 115

gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctctctcat 625
 Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
 120 125

ccctttcttc cctttgagca ttgccctctt tgggttcttt ttgagccaat tctaataaaa 685
 gtaaaaatgg taatagt 702

<210> 7
 <211> 233
 <212> PRT
 <213> Homo sapiens

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Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
 35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
 50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
 65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
 85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
 100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
 115 120 125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
 130 135 140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
 145 150 155 160
 Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
 165 170 175
 Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly
 180 185 190
 Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser
 195 200 205
 Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr
 210 215 220
 Pro Ser Gly Met Val Phe His Arg Val
 225 230

<210> 8
 <211> 2409
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (225).. (923)

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 cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccc 180
 aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
 Met Ala Gly Ala
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 att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
 Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
 5 10 15 20
 ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332
 Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
 25 30 35
 cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
 Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
 40 45 50
 gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
 Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
 55 60 65
 aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
 Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
 ile Glu Ala Asn Asp ile Val Phe Ser Val His ile Pro Leu Pro His
 85 90 95 100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572
 Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe ile Leu Gln Leu
 105 110 115

gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc 620
 Asp ile Ala Phe Lys Leu Asn Asn Gln ile Arg Glu Asn Ala Glu Val
 120 125 130

tcc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg 668
 Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp
 135 140 145

act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc 716
 Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe
 150 155 160

aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat 764
 Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp
 165 170 175 180

gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag 812
 Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu
 185 190 195

gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat 860
 Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His
 200 205 210

ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg 908
 Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met
 215 220 225

gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttggtga catccgacag 963
 Val Phe His Arg Val
 230

ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg 1023
 gatcagcacg agcggaacca catcgaggg tattggaagc aagtcggacc cattgccgtt 1083
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 ggtgggggtg ggggtgtattc cttgggggat ggtttgggcc gaatggggag tggaatattt 2043
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 tttttt 2409

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 <211> 198
 <212> PRT
 <213> Homo sapiens

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 Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
 35 40 45
 Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
 50 55 60
 Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
 65 70 75 80
 Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
 85 90 95

Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
 100 105 110
 Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
 115 120 125
 Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
 130 135 140
 Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
 145 150 155 160
 Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
 165 170 175
 Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
 180 185 190
 Arg His Val Val Leu Ser
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<210> 10
 <211> 1498
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> (86).. (679)

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 Met Ala Thr Leu Trp Gly Gly Leu Leu
 1 5
 cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160
 Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu
 10 15 20 25
 ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208
 Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg
 30 35 40
 tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256
 Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr
 45 50 55
 aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304
 Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu
 60 65 70
 ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352
 Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys
 75 80 85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att	400
Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile	
90 95 100 105	
ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat	448
Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr	
110 115 120	
ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca	496
Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala	
125 130 135	
cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca	544
Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala	
140 145 150	
aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg	592
Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu	
155 160 165	
aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag	640
Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu	
170 175 180 185	
cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa	689
Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser	
190 195	
ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actggggtttt	749
gctgggttttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact	809
ggaagcaaaaa acttgcttga ttttttttc ttgttaacgt aataatagag acatttttaa	869
aagcacacag ctcaaagtca gccataagt cttttcctat ttgtgacttt tactaataaa	929
aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc	989
accacatagt tttaacttga ctttcaagat aattttcagg gtttttggtg ttgttggttt	1049
ttgtttgttt gttttgggtg gagaggggag ggatgcctgg gaagtggta acaacttttt	1109
tcaagtcact ttactaaaca aacttttgta aatagacctt accttctatt ttcgagtttc	1169
atttatattt tgcagtgtag ccagcctcat caaagagctg acttactcat ttgacttttg	1229
cactgactgt attatctggg tatctgctgt gtctgcactt catggtaaac gggatctaaa	1289
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tgcatcctag aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg	1409
tgtgtgtggt cttactcatc ttctagtacc tttaaggaca aatcctaagg acttggacac	1469
ttgcaataaa gaaattttat tttaaacc	1498

<210> 11
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 11

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          20           25           30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu
          35           40           45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
          50           55           60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
          65           70           75           80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
          85           90           95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile
          100          105          110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe
          115          120          125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala
          130          135          140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp
          145          150          155          160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly
          165          170          175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe
          180          185          190

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Met Ala Leu Ala Leu Ala Ala
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Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro
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Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr
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Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr
60 65 70
aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413
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atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp
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Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met
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Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu
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tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605
Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser
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Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser
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Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
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Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
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Ala Lys Val Arg Lys Pro Glu Thr Phe Ser Asn Leu P Arg Thr
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 Arg Val Leu Phe Ile Tyr
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35 40 45
 Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50

55

60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
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 Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
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 100 105 110
 Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
 115 120 125
 Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
 130 135 140
 Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
 145 150 155 160
 Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
 165 170 175
 Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
 180 185 190
 Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
 195 200 205
 Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
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Tyr	Phe	Phe	Leu	Leu													
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 Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
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 Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
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Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala	
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Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Tyr Ser Ser Ile Thr	
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Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr	
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 Tyr Phe Phe Leu Leu
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Asn	Ala	Glu	Val	Ser	Ala	Ala	Ala	Ala	Gly	Ala	Thr	Gly	Ser	Glu	Glu
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Ala	Ala	Thr	Thr	Ser	Ser	Thr	Gly	Val	Ala	Val	Gly	Ala	Glu	His	Gly
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Glu	Asp	Ser	Leu	Ser	Arg	Lys	Pro	Asp	Pro	Glu	Pro	Gly	Arg	Met	Asp
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His	His	Gln	Pro	Gly	Thr	Gly	Arg	Tyr	Gln	Val	Leu	Leu	Asn	Glu	Glu
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Asp	Asn	Ser	Glu	Ser	Ser	Ala	Ile	Glu	Gln	Pro	Pro	Thr	Ser	Asn	Pro
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Tyr	Ser	Val	Ala	Thr	Ser	Leu	Pro	Thr	Tyr	Asp	Glu	Ala	Glu	Lys	Ala
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Lys	Ala	Ala	Ala	Met	Ala	Ala	Ala	Ala	Ala	Glu	Thr	Ser	Gln	Arg	Ile
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Gln	Glu	Glu	Glu	Cys	Pro	Pro	Arg	Asp	Asp	Phe	Ser	Asp	Ala	Asp	Gln
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Leu	Arg	Val	Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	Ala	Phe	Phe	Met	Ala
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Thr	Ile	Ala	Gly	Arg	Tyr	Gly	Ala	Ile	Cys	Gly	Phe	Gly	Leu	Ser	Leu
			260				265						270		
Ile	Lys	Trp	Ile	Leu	Ile	Val	Arg	Phe	Ser	Asp	Tyr	Phe	Thr	Gly	Tyr

275

280

285

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Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53).. (1060)

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 1

cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106
 Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
 5 10 15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
 Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
 20 25 30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202
 Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35 40 45 50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
 Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
 55 60 65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct tct tca gca cca gca ctt gaa gac tct Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser	490
135 140 145	
tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser	538
150 155 160	
gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser	586
165 170 175	
gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala	634
180 185 190	
gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu	682
195 200 205 210	
gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg	730
215 220 225	
gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile	778
230 235 240	
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile	826
245 250 255	
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys	874
260 265 270	
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn	922
275 280 285 290	
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu	970
295 300 305	
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu	1018
310 315 320	
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu	1060
325 330 335	
tagagactgc atcaaccgga cattcctttc ttataccaat gtgaaatttc cagatcatct	1120
gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag	1180
acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc	1240

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 gcatatactt gatagaaacc ataaagtgt agcagttaag tccagtcaca ttgtgtaaat 1360
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 accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900
 ttttcagatg ggaagctgca ttttaggat tgcccatctt aagagatctt gcaggaagag 1960
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 attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500
 actactaaaa ggtacatcta actattcagg gacatttttc catttcaaaa aaataaaatt 2560
 tattatgott tataacctct tctgtatttt ctaatttttt cattgtcttt gataaataaa 2620
 acagttttgt ttigct 2636

<210> 19
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 19
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 1 5 10 15

Leu Asn Ser Ala Arg Ty Ala Pro Glu Leu Leu Arg Gly T Ala Thr
 20 25 30
 Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
 35 40 45
 Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
 50 55 60
 Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
 65 70 75 80
 Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
 85 90 95
 His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
 100 105 110
 Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
 115 120 125
 Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
 130 135 140
 Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
 145 150 155 160
 Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
 165 170 175
 Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
 180~ 185 190
 Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
 195 200 205
 Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
 210 215 220
 Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
 225 230 235 240
 Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
 245 250 255
 Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
 260 265 270
 Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
 275 280 285
 Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
 290 295 300
 Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
 305 310 315 320
 Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

<210> 20
 <211> 2636
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (53).. (1060)

<400> 20

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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106
 Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
 5 10 15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
 Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
 20 25 30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202
 Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35 40 45 50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
 Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
 55 60 65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586

Asp Thr Glu Val Tyr	Glu Phe Tyr Pro Val Pro Pro	Tyr Ser	
165	170	175	
gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct			634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala			
180	185	190	
gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag			682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu			
195	200	205	210
gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga			730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg			
	215	220	225
gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att			778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile			
	230	235	240
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata			826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile			
	245	250	255
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa			874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys			
	260	265	270
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat			922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn			
	275	280	290
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt			970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu			
	295	300	305
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa			1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu			
	310	315	320
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg			1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu			
	325	330	335
tagagactgc atcaaccoga cattcctttc ttataccaat gtgaaatttc cagatcatct			1120
gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag			1180
acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc			1240
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gcatatactt gatagaaacc ataaagtgt agcagttaag tccagtcaca tttggttaat			1360
cagtgtttga tataattgaa agagttgagt ggataaacag tcttcagct tgtaaagcc			1420
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taaggtgtat tgaacctgc agtgctgatt attagaaagg attgtgcaga tttttgaaca 1600
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 accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900
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 tatctttgggt ttggaatacc aacatttaaa atgatgggtat tttatctttt aaacttaaaa 2440
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 actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560
 tattatgctt tataacctct tctgtatttt ctaatttttt cattgtcttt gataaataaa 2620
 acagttttgt tttgct 2636

<210> 21

<211> 76

<212> PRT

<213> Homo sapiens

<400> 21

Met	Val	Cys	Ile	Pro	Cys	Ile	Val	Ile	Pro	Val	Leu	Leu	Trp	Ile	Tyr
1				5					10					15	

Lys	Lys	Phe	Leu	Glu	Pro	Tyr	Ile	Tyr	Pro	Leu	Val	Ser	Pro	Phe	Val
			20					25					30		

Ser	Arg	Ile	Trp	Pro	Lys	Lys	Ala	Ile	Gln	Glu	Ser	Asn	Asp	Thr	Asn
		35					40					45			

Lys	Gly	Lys	Val	Asn	Phe	Lys	Gly	Ala	Asp	Met	Asn	Gly	Leu	Pro	Thr
	50					55					60				

Lys Gly Pro Thr Glu Cys Asp Lys Lys Lys Asp
65 70 75

<210> 22
<211> 1085
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (176).. (403)

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gcagagtcct aggcggtgcg cggcctcctg cctcctccct cctcggcggt cgcgccccgc 120
cggcctccgc ggtgcctgcc ttgcctctca ggttgaggag ctcaagcttg ggaaa atg 178
Met
1
gtg tgc att cct tgt atc gtc att cca gtt ctg ctg tgg atc tac aaa 226
Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys
5 10 15
aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274
Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser
20 25 30
cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322
Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys
35 40 45
ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370
Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys
50 55 60 65
gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttctaaagg 423
Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
70 75
accccatcat ttaaaaaatg gacctgataa tatgaagcat cticcttgta attgtctctg 483
acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaadc 543
aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaaatga cctcattcct 603
aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663
aaatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723
ttctctaatt catatgaatt tgctgtttgc tctaatttct ttgggctcct ctaatttgag 783
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ttttgggagg taataatgat gtgaaacata aagatttaat aattactgtc caacacagtg 903

gagcagcttg tccacaaa tagtaattac tatttattgc tctaaggaa ttttaaaaaa 963
 gatagggaag aggggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtcta 1023
 tataaaattt taatccttac tgcatttctt ctgttcctac aaatgtatta aacattcagt 1083
 tt 1085

<210> 23
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 23
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 1 5 10 15
 Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
 20 25 30
 Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
 35 40 45
 Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
 50 55 60
 Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
 65 70 75 80
 Leu Ser Gly Leu

<210> 24
 <211> 1593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (65).. (316)

<400> 24
 agcgtcgcct cagcgcggagc agagctgagc tgaagcggga cccggagccc gagcagccgc 60
 cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109
 Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile
 1 5 10 15
 ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157
 Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys
 20 25 30
 gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205
 Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln
 35 40 45

att ccc ctg ttt ggg c atg tct tca gat tca gct gac c ttc tat 253
 Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr
 50 55 60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301
 Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His
 65 70 75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356
 Ser Leu Ser Gly Leu
 80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggcttttagac 416
 attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt 476
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 gccccaggct cctccatatg gcccagggt taccacccta tcacacgtgg ccttgtctag 1196
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 aaggcaccag gcctcaggag gagccccata gtcccgctg cagcctgtaa ccatcggctg 1436
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<210> 25
 <211> 179
 <212> PRT

<213> Homo sapiens

<400> 25

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
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Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
50 55 60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
65 70 75 80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
85 90 95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
100 105 110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
115 120 125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
130 135 140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr
145 150 155 160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala
165 170 175

Leu Leu Phe

<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114).. (650)

<400> 26

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acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116
Met
1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164
Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212
 Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu
 20 25 30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260
 Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro
 35 40 45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308
 Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val
 50 55 60 65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356
 Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr
 70 75 80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404
 Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu
 85 90 95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452
 Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val
 100 105 110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500
 His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu
 115 120 125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548
 Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
 130 135 140 145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596
 Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
 150 155 160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644
 Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
 165 170 175

ctc ttc tgagccgctc tcccggacag gttgaggaag ctgctccaga agcgccctcg 700
 Leu Phe

aaggggagct ctcatcatgg cgcgtgctgc tgcggcatat ggacttttaa taatgttttt 760

gaatttcgta ttctttcatt ccactgtgta aagtgtctaga cattttccaa tttaaaattt 820

tgctttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

cagagaagtg ggaatggat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

tttgcacctt ctcaagtgtg tatgaggctg cagccgtctc acctgtttcc ccacaaaggg 1000

aatttctcac tctggttgga agcacaacaa ctgaaatgtc tacgtttcat tttggcagta 1060

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60
 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110
 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
 115 120 125
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
 130 135 140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
 145 150 155 160
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
 165 170 175
 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
 180 185 190
 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
 195 200 205
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
 210 215 220
 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
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 260 265 270
 Ile Ala Lys Val Lys Ala Asn
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 <213> Homo sapiens

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 atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15
 ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30
 tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262
 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60

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Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe	
65 70 75 80	
ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg	406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val	
85 90 95	
gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg	454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp	
100 105 110	
ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt	502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe	
115 120 125	
att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat	550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His	
130 135 140	
cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg	598
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro	
145 150 155 160	
gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc	646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val	
165 170 175	
ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa	694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln	
180 185 190	
ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag	742
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln	
195 200 205	
ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc	790
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser	
210 215 220	
tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc	838
Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly	
225 230 235 240	
acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc	886
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr	
245 250 255	
aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt	934
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly	
260 265 270	
att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgccacc	985
Ile Ala Lys Val Lys Ala Asn	
275	
taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct	1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct cccacagct 1105
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 <212> PRT
 <213> Homo sapiens

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 Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
 35 40 45
 Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
 50 55 60
 Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 65 70 75 80
 Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
 85 90 95
 Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
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 Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
 115 120 125
 Tyr Met Asp Ala Pro Lys Ala Ala Leu
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<210> 30
 <211> 1788
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (145).. (555)

<400> 30

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ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171
                               Met Gly Phe Gly Ala Thr Leu Ala Val
                               1                               5
ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219
Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
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acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267
Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
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gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315
Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
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cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363
Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
                               60                               65                               70
tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411
Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
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Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
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Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
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cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555
Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
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agatgtgtcc tggtttcg agcgtagcca gctgctgctt gaggccatg tcgtccccg 1035
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<210> 31
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
 50 55 60
 Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 65 70 75 80
 Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
 85 90 95
 Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
 100 105 110
 Glu Cys Pro Cys Gln Leu
 115

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<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

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Pro	Pro	Tyr	Thr	Asp	Ala	Pro	Pro	Ala	Tyr	Ser	Glu	Leu	Tyr	Arg	Pro
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Ser	Phe	Val	His	Pro	Gly	Ala	Ala	Thr	Val	Pro	Thr	Met	Ser	Ala	Ala
	50					55					60				

Phe	Pro	Gly	Ala	Ser	Leu	Tyr	Leu	Pro	Met	Ala	Gln	Ser	Val	Ala	Val
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80

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	Met	Asn	Ser	Lys	Gly	Gln	Tyr	Pro	Thr	Gln	Pro	Thr	Tyr	Pro						
	1				5					10										
gtg	cag	cct	cct	ggg	aat	cca	gta	tac	cct	cag	acc	ttg	cat	ctt	cct	159				
Val	Gln	Pro	Pro	Gly	Asn	Pro	Val	Tyr	Pro	Gln	Thr	Leu	His	Leu	Pro					
15					20					25					30					
cag	gct	cca	ccc	tat	acc	gat	gct	cca	cct	gcc	tac	tca	gag	ctc	tat	207				
Gln	Ala	Pro	Pro	Tyr	Thr	Asp	Ala	Pro	Pro	Ala	Tyr	Ser	Glu	Leu	Tyr					
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cgt	ccg	agc	ttt	gtg	cac	cca	ggg	gct	gcc	aca	gtc	ccc	acc	atg	tca	255				
Arg	Pro	Ser	Phe	Val	His	Pro	Gly	Ala	Ala	Thr	Val	Pro	Thr	Met	Ser					
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		65					70					75								
gct	gtt	ggg	cct	tta	ggt	tcc	aca	atc	ccc	atg	gct	tat	tat	cca	gtc	351				
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Gly Pro Ile Tyr Pro Gly Ser Thr Val Leu Val Glu Gly Tyr
 95 100 105 110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
 Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
 115 120 125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
 Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
 130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543
 Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
 145 150 155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593
 Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp
 160 165

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<210> 35
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 <212> PRT
 <213> Homo sapiens

<400> 35
 Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu
 1 5 10 15
 Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
 20 25 30
 Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
 35 40 45
 Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
 50 55 60
 Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
 65 70 75 80
 Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
 85 90 95
 Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
 100 105 110
 Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
 115 120 125
 Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
 130 135 140
 Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
 145 150 155 160
 Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
 165 170 175
 Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
 180 185 190
 Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
 195 200 205
 Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
 210 215 220
 Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
 225 230 235 240
 Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
260 265 270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
275 280 285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
290 295 300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305 310 315 320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
325 330 335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
340 345 350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
355 360 365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
370 375 380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
385 390 395 400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
405 410 415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
420 425 430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
435 440 445

Pro Glu Lys Gln Met Ala Pro
450 455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS



<222> (116).. (1480)

<400> 36

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tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118

Met
1

agt ttc ctc atc gac  agc atc atg att acc tcc cag a  cta ttt	166
Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe	
5 10 15	
ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat	214
Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr	
20 25 30	
gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca	262
Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala	
35 40 45	
ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta	310
Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val	
50 55 60 65	
ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta	358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val	
70 75 80	
att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt	406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe	
85 90 95	
att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc	454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser	
100 105 110	
tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat	502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp	
115 120 125	
ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag	550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln	
130 135 140 145	
ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt	598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu	
150 155 160	
tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc	646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe	
165 170 175	
ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg	694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu	
180 185 190	
ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg	742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met	
195 200 205	
gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca	790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser	
210 215 220 225	
ggg ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt	838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser	

gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu	886
245 250 255	
agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu	934
260 265 270	
aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu	982
275 280 285	
ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr	1030
290 295 300 305	
atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg	1078
310 315 320	
ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys	1126
325 330 335	
ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val	1174
340 345 350	
aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala	1222
355 360 365	
atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln	1270
370 375 380 385	
ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser	1318
390 395 400	
atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu	1366
405 410 415	
cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser	1414
420 425 430	
gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro	1462
435 440 445	
gag aag caa atg gca cct tgaacttaag cctactacag actgtagag Glu Lys Gln Met Ala Pro	1510
450 455	

gccagtgggtt tcaaaattgatataagag gggggaaaaa tggaaccagcctgacatt 1570
 ttataaaciaa acaaaatgct atggtagcat tttcacctt catagcatac tccttccccg 1630
 tcaggtgata ctatgacat gagtagcatc agccagaaca tgagaggag aactaactca 1690
 agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggaggagagg 1750
 agccaagaaa ctaaaggatga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810
 gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaaaagggt tatagctttg 1870
 ccttgagatt gactcattaa aatcagagac tgt 1903

<210> 37
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 37
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 Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
 20 25 30
 Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser
 35 40 45
 Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile
 50 55 60
 Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
 65 70 75 80
 His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met
 85 90 95
 Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala
 100 105 110
 Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
 115 120 125
 Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
 130 135 140
 Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu
 145 150 155 160
 Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
 165 170 175
 Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
 180 185 190
 Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
 210 215 220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
 225 230 235 240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
 245 250 255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
 260 265 270

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
 275 280 285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
 290 295 300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
 305 310 315 320

Phe Gln

<210> 38
 <211> 1448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (292).. (1257)

<400> 38
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 tcggagagcc gagtgaagac atttcacct ggacacctga ccatgtgcct gccctgagca 180
 gcgaggccca ccaggcatct ctgttgtggg cagcagggcc aggtcctggt ctgtggaccc 240
 tcggcagttg gcaggctccc tctgcagtgg ggtctgggcc tcggccccac c atg tcg 297
 Met Ser
 1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345
 Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser
 5 10 15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393
 Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala
 20 25 30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441

Ala 35	Asp	Lys	Ser	Ala	Val	Ala	Ala	Ala	Ala	Pro	Ala	Val	Ala	50		
					40				45							
gat	gac	aca	cca	ccc	ccc	gag	cgt	cgg	aac	aag	agc	ggt	atc	atc	agt	489
Asp	Asp	Thr	Pro	Pro	Pro	Glu	Arg	Arg	Asn	Lys	Ser	Gly	Ile	Ile	Ser	
				55					60				65			
gag	ccc	ctc	aac	aag	agc	ctg	cgc	cgc	tcc	cgc	ccg	ctc	tcc	cac	tac	537
Glu	Pro	Leu	Asn	Lys	Ser	Leu	Arg	Arg	Ser	Arg	Pro	Leu	Ser	His	Tyr	
			70				75					80				
tct	tct	ttt	ggc	agc	agt	ggt	ggt	agt	ggc	ggt	ggc	agc	atg	atg	ggc	585
Ser	Ser	Phe	Gly	Ser	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Met	Met	Gly	
		85				90						95				
gga	gag	tct	gct	gac	aag	gcc	act	gcg	gct	gca	gcc	gct	gcc	tcc	ctg	633
Gly	Glu	Ser	Ala	Asp	Lys	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Ser	Leu	
	100					105					110					
ttg	gcc	aat	ggg	cat	gac	ctg	gcg	gcg	gcc	atg	gcg	gtg	gac	aaa	agc	681
Leu	Ala	Asn	Gly	His	Asp	Leu	Ala	Ala	Ala	Met	Ala	Val	Asp	Lys	Ser	
	115				120					125					130	
aac	cct	acc	tca	aag	cac	aaa	agt	ggt	gct	gtg	gcc	agc	ctg	ctg	agc	729
Asn	Pro	Thr	Ser	Lys	His	Lys	Ser	Gly	Ala	Val	Ala	Ser	Leu	Leu	Ser	
				135					140				145			
aag	gca	gag	cgg	gcc	acg	gag	ctg	gca	gcc	gag	gga	cag	ctg	acg	ctg	777
Lys	Ala	Glu	Arg	Ala	Thr	Glu	Leu	Ala	Ala	Glu	Gly	Gln	Leu	Thr	Leu	
			150					155					160			
cag	cag	ttt	gcg	cag	tcc	aca	gag	atg	ctg	aag	cgc	gtg	gtg	cag	gag	825
Gln	Gln	Phe	Ala	Gln	Ser	Thr	Glu	Met	Leu	Lys	Arg	Val	Val	Gln	Glu	
		165					170					175				
cat	ctc	ccg	ctg	atg	agc	gag	gcg	ggt	gct	ggc	ctg	cct	gac	atg	gag	873
His	Leu	Pro	Leu	Met	Ser	Glu	Ala	Gly	Ala	Gly	Leu	Pro	Asp	Met	Glu	
	180					185					190					
gct	gtg	gca	ggt	gcc	gaa	gcc	ctc	aat	ggc	cag	tcc	gac	ttc	ccc	tac	921
Ala	Val	Ala	Gly	Ala	Glu	Ala	Leu	Asn	Gly	Gln	Ser	Asp	Phe	Pro	Tyr	
	195				200					205					210	
ctg	ggc	gct	ttc	ccc	atc	aac	cca	ggc	ctc	ttc	att	atg	acc	ccg	gca	969
Leu	Gly	Ala	Phe	Pro	Ile	Asn	Pro	Gly	Leu	Phe	Ile	Met	Thr	Pro	Ala	
				215					220					225		
ggt	gtg	ttc	ctg	gcc	gag	agc	gcg	ctg	cac	atg	gcg	ggc	ctg	gct	gag	1017
Gly	Val	Phe	Leu	Ala	Glu	Ser	Ala	Leu	His	Met	Ala	Gly	Leu	Ala	Glu	
			230					235					240			
tac	ccc	atg	cag	gga	gag	ctg	gcc	tct	gcc	atc	agc	tcc	ggc	aag	aag	1065
Tyr	Pro	Met	Gln	Gly	Glu	Leu	Ala	Ser	Ala	Ile	Ser	Ser	Gly	Lys	Lys	
		245					250					255				
aag	cgg	aaa	cgc	tgc	ggc	atg	tgc	gcg	ccc	tgc	cgg	cgg	cgc	atc	aac	1113
Lys	Arg	Lys	Arg	Cys	Gly	Met	Cys	Ala	Pro	Cys	Arg	Arg	Arg	Ile	Asn	
	260					265					270					

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161
 Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile 290
 275 280 285
 tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209
 Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala 305
 295 300
 ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257
 Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln 320
 310 315
 tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317
 agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377
 tcacagattt cattcctgtt tttatatata tattttttgt tgtcgtttta acatctccac 1437
 gtccctagca t 1448

<210> 39
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 39
 Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn
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 Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu
 35 40 45
 Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys
 50 55 60
 Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu
 65 70 75 80
 Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
 85 90 95
 Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
 100 105 110
 Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
 115 120 125
 Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
 130 135 140
 Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
 145 150 155 160

Glu His Met His Ser Arg Val Met His Arg Asp Ile Pro Ala
 165 170 175
 Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
 180 185 190
 Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
 195 200 205
 Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
 210 215 220
 Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
 225 230 235 240
 Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
 245 250 255
 Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
 260 265 270
 His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
 275 280 285
 Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
 290 295 300
 Gln Met His Ile Trp Met Ser Ser Thr
 305 310

<210> 40
 <211> 1597
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (153).. (1091)

<400> 40
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 ctccagccgc ccgcggggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120
 ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173
 Met Ala Gly Gln Pro Gly His
 1 5
 atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221
 Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro
 10 15 20
 gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269
 Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg
 25 30 35
 tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317

Cys Ser Leu Ala Asp	Gln Ile Glu Lys Lys Ile Gly A	Gly Gln	
40	50	55	
ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg	365		
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val			
60	65	70	
gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg	413		
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg			
75	80	85	
cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca	461		
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro			
90	95	100	
aat atc atc aag tat ttg gac tgc ttt atc gaa gac aac gag ctg aac	509		
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn			
105	110	115	
att gtg ctg gag ttg gct gac gca ggg gac ctc tgc cag atg atc aag	557		
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys			
120	125	130	135
tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag	605		
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys			
140	145	150	
tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg	653		
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg			
155	160	165	
gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg	701		
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr			
170	175	180	
ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct	749		
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser			
185	190	195	
gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca	797		
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser			
200	205	210	215
ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg	845		
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp			
220	225	230	
tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc	893		
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe			
235	240	245	
tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag	941		
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln			
250	255	260	
tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga	989		
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg			
265	270	275	

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037
 Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
 280 285 290 295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085
 Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
 300 305 310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac ttgccttac 1141
 Ser Thr

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201

tcagcagggt ccccaaaagg ctgccagcc ttacagcaga tgctgaaggc agagcagctg 1261

agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttggtgaca atctcagctg ggtcaataag ggcaggtggt tcagcgagcc acggcagccc 1381

cctgtatctg gattgtaatg tgaatcttta gggtaatcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttggt tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggt tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
 1 5 10 15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr
 20 25 30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
 35 40 45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
 50 55 60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
 65 70 75 80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
 85 90 95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
 100 105 110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
 115 120 125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
 130 135 140
 Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
 145 150 155 160
 Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
 165 170 175
 Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
 180 185 190
 Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
 195 200 205
 Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
 210 215 220
 Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
 225 230 235 240
 Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
 245 250 255
 Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
 260 265 270
 Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
 275 280 285
 Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
 290 295 300
 Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
 305 310 315 320
 Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
 325 330 335
 Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
 340 345 350
 Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
 355 360 365
 Ala Lys Glu
 370

<210> 42
 <211> 1781
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91).. (1203)

<400> 42

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ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114
Met Ser His Glu Lys Ser Phe Leu
1 5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162
Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly
10 15 20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210
Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
25 30 35 40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258
Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
45 50 55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306
Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
60 65 70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354
Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
75 80 85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402
Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
90 95 100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
105 110 115 120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546
Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
140 145 150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg 594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val
155 160 165

ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act 642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr
170 175 180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac 690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr
185 190 195 200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt 738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg 786
 Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser
 220 225 230

gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc 834
 Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe
 235 240 245

tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc 882
 Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
 250 255 260

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930
 Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
 265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978
 Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
 285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026
 Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
 300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074
 Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
 315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122
 Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
 330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170
 Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
 345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
 Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
 365 370

gtgcccgtc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttcccct ctctcttgtc ccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343

ctctgtatg tacactgcag atacttccat ttggaccgcg tgtggccaca gcatggcccc 1403

tttagtctc cgcggccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463

tactcattgt tgcattgagc ctgtctgcca gccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaaagggt gaggggtgcac gtcttccctc ctgtcccagc 1583

tccccagcct ggcgtagagc acccctcccc tccccccac cccctggag tgctgcccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

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tgggatttgc tctctgcc

1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
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Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
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Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
 260 265 270
 Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
 275 280 285
 Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
 290 295 300
 Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
 305 310 315 320
 Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
 325 330 335
 Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
 340 345 350
 His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
 355 360 365
 Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
 370 375 380
 Leu Val Pro Gly Pro Glu Lys Glu Asn
 385 390

<210> 44
 <211> 2396
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50).. (1228)

<400> 44
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 Met Ser Asp
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gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
 Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
 5 10 15
 cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
 Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20 25 30 35
 gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202
 Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
 40 45 50
 gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
 Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
 55 60 65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu	298
70 75 80	
cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu	346
85 90 95	
tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala	394
100 105 110 115	
ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly	442
120 125 130	
gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val	490
135 140 145	
act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe	538
150 155 160	
gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val	586
165 170 175	
ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His	634
180 185 190 195	
atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr	682
200 205 210	
gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu	730
215 220 225	
gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr	778
230 235 240	
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile	826
245 250 255	
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu	874
260 265 270 275	
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu	922
280 285 290	
acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat	970

Thr Gly Pro Lys Arg ████████ n Leu Met Ala Leu Ala Arg Thr ████████ Trp Asn
 295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018
 Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
 310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066
 Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
 325 330 335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
 Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
 340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
 360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
 375 380 385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258
 Gly Pro Glu Lys Glu Asn
 390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct ccctcccccg aagtctcttg tggatgatgac cgctctcccc 1378

tgccccctccc cgcttccctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaaag gcgacaggga gggtcagagg gaggccggct gcttccctgcc ccacccttt 1498

ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtccccctg ttgtgttcca 1558

tgtgctttca cctctgcctc atctttcctc ccgtccctgc cccgccacct ccccaaagaa 1618

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cctcatcgtg gtctgtgcca tgtcccgctt ctatggtggt tgaggagaaa ggcggggaag 1918

cttcctcagc ctgacagata tgtgtggcat ttactagcca gagctctgaa aggagtgct 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttctc aaactcagcc caaaactctg 2098

tttacatggg tggggagatg gagcaggga gtacagagt ggatggtcag gacctgggcc 2158

attgcaacca aaatggggac ttctgggta gggaggtcac tccctctact cactgagcta 2218

ggattagga gggttattgc cccaaccatt gcaatgggag gtggaggac aggctcagcc 2278
 tcctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338
 accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
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 Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
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 Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
 35 40 45
 Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
 50 55 60
 Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
 65 70 75 80
 Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
 85 90 95
 Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
 100 105 110
 Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
 115 120 125
 Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
 130 135 140
 Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
 145 150 155 160
 Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
 165 170 175
 Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
 180 185 190
 Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
 195 200 205
 Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
 210 215 220
 Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
 225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
 245 250 255
 Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
 260 265 270
 Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
 275 280 285
 Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
 290 295 300
 Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
 305 310 315 320
 Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
 325 330 335
 Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
 340 345 350
 His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
 355 360 365
 Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
 370 375 380
 Leu Val Pro Gly Pro Glu Lys Gln Asn
 385 390

<210> 46
 <211> 2396
 <212> DNA
 <213> Homo sapiens



<220>
 <221> CDS
 <222> (50)..(1228)

<400> 46
 agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58
 Met Ser Asp
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gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
 Glu Arg Glu Val Ala Glu Ala Thr Gly Glu Asp Ala Ser Ser Pro
 5 10 15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
 Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20 25 30 35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202
 Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
 40 45 50

gtg ctc acc ggc ttt  ggc tac gac aag gtg aag ctg  agc cgg	250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg	
55 60 65	
ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg	298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu	
70 75 80	
cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg	346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu	
85 90 95	
tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg	394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala	
100 105 110 115	
ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga	442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly	
120 125 130	
gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg	490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val	
135 140 145	
act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt	538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe	
150 155 160	
gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc	586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val	
165 170 175	
ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac	634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His	
180 185 190 195	
atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca	682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr	
200 205 210	
gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag	730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu	
215 220 225	
gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act	778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr	
230 235 240	
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att	826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile	
245 250 255	
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc	874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu	
260 265 270 275	
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg	922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu	

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
 Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
 295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018
 Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
 310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066
 Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
 325 330 335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
 Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
 340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
 360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
 375 380 385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258
 Gly Pro Glu Lys Gln Asn
 390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318
 ctgtcataat gctctgccct ccctcccccg aagttctctg tggatgatgac cgctctcccc 1378
 tgccccctccc cgcttctctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438
 ccctgccaaag gcgacaggga gggctcagagg gaggccggct gcttctctgcc cccacccttt 1498
 ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtccccctg ttgtgttcca 1558
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 atctcgtcct ctgtcccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798
 ctgccattct taaccaaggc agccccaagc ctcttgggga ggcagggcaa aaacaggtgc 1858
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<212> PRT
<213> Homo sapiens

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Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
35 40 45
Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
50 55 60
Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
65 70 75 80
Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
85 90 95
Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
100 105 110
Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
115 120 125
Asp Lys Val Gly Glu Ser Asn Asn Met Val
130 135

<210> 48
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<212> DNA
<213> Homo sapiens

<220>
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tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166
 Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val
 5 10 15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214
 Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu
 20 25 30 35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262
 Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly
 40 45 50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310
 Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala
 55 60 65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358
 Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro
 70 75 80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406
 Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg
 85 90 95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454
 Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
 100 105 110 115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502
 Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
 120 125 130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553
 Gly Glu Ser Asn Asn Met Val
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aaatattgtg ttatttataa agtcatttga agaattattca gcacaaaatt aaattacatg 613
 aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673
 caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733
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2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

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His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
20 25 30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
35 40 45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
50 55 60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
65 70 75 80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
85 90 95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser
100 105 110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
115 120 125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
130 135 140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145 150 155 160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
165 170 175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
180 185 190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
195 200 205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
210 215 220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
225 230 235 240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
260 265 270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
275 280 285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
290 295 300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
305 310 315 320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
325 330 335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
340 345 350

Arg Ser Thr Thr His Leu Ile
355

<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

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<222> (327).. (1403)

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aacgtggtgg acctatcctt gcaccagagg agattaagac tatttttgggt agcatcccg 180
atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240
atgagagcaa aagcattggg gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300
acctccctt tgtaaacttc ttgaa atg agc aag gaa aca att att aaa tgt 353
Met Ser Lys Glu Thr Ile Ile Lys Cys
1 5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401
Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala
10 15 20 25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449
Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro
30 35 40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497
Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile 60 65 70	545
gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys 75 80 85	593
aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly 90 95 100 105	641
tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val 110 115 120	689
gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val 125 130 135	737
act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His 140 145 150	785
aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro 155 160 165	833
gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys 170 175 180 185	881
gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu 190 195 200	929
ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln 205 210 215	977
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cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile 235 240 245	1073
tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp 250 255 260 265	1121
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gtt aca aga gca ttc ttc tcc aaa act cca aaa aga gct ctt cga 1217
 Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg
 285 290 295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265
 Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser
 300 305 310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313
 Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu
 315 320 325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361
 Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu
 330 335 340 345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata 1403
 Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
 350 355

tgaagcgtaa ccaaaatctt aaattataga aatgtataga cacctcatatc tcaaataaga 1463
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2636

<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

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Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
35 40 45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
50 55 60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65 70 75 80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
85 90 95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
100 105 110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
115 120 125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
130 135 140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
145 150 155 160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
165 170 175

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
180 185 190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
195 200 205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
210 215 220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
225 230 235 240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
245 250 255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu
 260 265 270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys
 275 280 285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu
 290 295 300

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
 305 310 315 320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
 325 330 335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
 340 345 350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
 355 360 365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
 370 375 380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
 385 390 395 400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
 405 410 415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
 420 425 430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
 435 440 445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
 450 455 460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
 465 470 475 480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
 485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
 500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
 515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
 530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
 545 550 555 560

Leu Leu Ile Arg Pro ████ Gln Arg Leu Pro Ser Val Ala ████ Leu Leu
 565 570 575
 Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
 580 585 590
 Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
 595 600 605
 Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
 610 615 620
 Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
 625 630 635 640
 Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
 645 650 655
 Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
 660 665 670
 Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
 675 680 685
 Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
 690 695 700
 Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
 705 710 715 720
 Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val
 725 730 735
 Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp
 740 745 750
 Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp
 755 760 765
 Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
 770 775 780
 Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
 785 790 795 800
 Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
 805 810 815
 Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu
 820 825 830
 Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
 835 840 845
 Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
 850 855 860
 Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr

His Leu Ile

<210> 52
 <211> 3910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (29).. (2677)

<400> 52

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tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct      100
Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser
    10                               15                               20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca      148
Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser
    25                               30                               35                               40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt      196
Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val
                               45                               50                               55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att      244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile
                               60                               65                               70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg      292
Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu
    75                               80                               85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat      340
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp
    90                               95                               100

tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca      388
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro
   105                               110                               115                               120

cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca      436
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser
    125                               130                               135

tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt      484
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe
    140                               145                               150

act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc      532
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val

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cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr 170 175 180	580
cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val 185 190 195 200	628
agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp 205 210 215	676
gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg 220 225 230	724
aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu 235 240 245	772
gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met 250 255 260	820
caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu 265 270 275 280	868
gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys 285 290 295	916
aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met 300 305 310	964
gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr 315 320 325	1012
cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn 330 335 340	1060
agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser 345 350 355 360	1108
aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala 365 370 375	1156
gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro 380 385 390	1204

gag tct agc att aa t gga gac acc cca aag tct tgt aag tct Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser 395 400 405	1252
tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln 410 415 420	1300
gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu 425 430 435 440	1348
gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln 445 450 455	1396
cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly 460 465 470	1444
agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu 475 480 485	1492
gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile 490 495 500	1540
ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val 505 510 515 520	1588
aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln 525 530 535	1636
aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu 540 545 550	1684
tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg 555 560 565	1732
tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala 570 575 580	1780
gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu 585 590 595 600	1828
aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala 605 610 615	1876
caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala	1924

aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile 635 640 645	1972
tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Val Thr Leu Phe 650 655 660	2020
ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile 665 670 675 680	2068
ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu 685 690 695	2116
aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp 700 705 710	2164
ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg 715 720 725	2212
cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser 730 735 740	2260
gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val 745 750 755 760	2308
gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala 765 770 775	2356
gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu 780 785 790	2404
agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg 795 800 805	2452
gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu 810 815 820	2500
atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp 825 830 835 840	2548
aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile 845 850 855	2596

cct tct ccc tcc ctt c agc ctt cct tcc ttc ttt gaa a aga agt 2644
 Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser
 860 865 870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgta ccaaaatctt 2697
 His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
 875 880

aaattataga aatgtataga cacctcatatc tcaaataaga aactgactta aatggtactt 2757
 gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817
 tttttcttct tgaaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa 2877
 atgatagtga ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937
 ttttaagttgc tatcagctga tattagtagc tttgcaacc tgaatagagta aataaatttt 2997
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 aaaacaagat gttttagct gtttcagaga gactacggta ttttatggt aattttatcc 3417
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 tgggaaaatt gtggtaaaga ctgtttgtac ctttcatgaa ataattctga agttgccatc 3537
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 cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657
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5

10

15

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 Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser
 35 40 45
 Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg
 50 55 60
 Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
 65 70 75 80
 Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
 85 90 95
 Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly
 100 105 110
 Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
 115 120 125
 Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
 130 135 140
 Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
 145 150 155 160
 His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
 165 170 175
 Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
 180 185 190
 Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
 195 200 205
 Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
 210 215 220
 Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly
 225 230 235 240
 Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met
 245 250 255
 Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
 260 265 270
 Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln
 275 280 285
 Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp
 290 295 300
 Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
 305 310 315 320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg
 325 330 335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu
 340 345 350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe
 355 360 365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile
 370 375 380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
 385 390 395 400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
 405 410 415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu
 420 425 430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
 435 440 445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
 450 455 460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
 465 470 475 480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
 485 490 495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
 500 505 510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
 515 520 525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
 530 535 540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
 545 550 555 560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
 565 570 575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
 580 585 590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr
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Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val
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<400> 54

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115
 Met Glu Gly Pro
 1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163
 Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro
 5 10 15 20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211
 Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala
 25 30 35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259
 Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp
 40 45 50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307
 Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu
 55 60 65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355
 Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser
 70 75 80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403
 Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
 85 90 95 100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451
 Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
 105 110 115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499
 Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
 120 125 130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547
 Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
 135 140 145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595
 Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
 150 155 160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643

Ile Ala Tyr Leu Ile	Lys Gly Gln Ser Val Asn Met Thr Asp Val	
165	170 175 180	
aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca	Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro	691
	185 190 195	
gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt	Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val	739
	200 205 210	
gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga	Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly	787
	215 220 225	
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat	Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp	835
	230 235 240	
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac	Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn	883
	245 250 255 260	
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga	Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg	931
	265 270 275	
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc	Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu	979
	280 285 290	
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac	Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr	1027
	295 300 305	
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta	Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu	1075
	310 315 320	
gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg	Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly	1123
	325 330 335 340	
tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt	Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val	1171
	345 350 355	
ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca	Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala	1219
	360 365 370	
gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta	Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu	1267
	375 380 385	
tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct	Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala	1315
	390 395 400	

tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc	1363
Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly	
405 410 415 420	
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Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro	
425 430 435	
tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat	1459
Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr	
440 445 450	
gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat	1507
Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His	
455 460 465	
cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg	1555
His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp	
470 475 480	
att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca	1603
Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr	
485 490 495 500	
ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt	1651
Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys	
505 510 515	
tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca	1699
Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser	
520 525 530	
tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg	1747
Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu	
535 540 545	
ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat	1795
Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His	
550 555 560	
atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc	1843
Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe	
565 570 575 580	
atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg	1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val	
585 590 595	
aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac	1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His	
600 605 610	
cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa	1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val	
615 620	
ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaaag tgaagtaaag	2049

atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa 2109
 aagttctcaa taaaggcatt acaatttttt aggttttagaa agatggactt ttctgataaa 2169
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 gtttcaaaat agtactattc tttaaacttg taatttttgc taagttatit gtctttgttg 2349
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 Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
 35 40 45
 Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
 50 55 60
 Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65 70 75 80
 Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
 85 90 95
 Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly
 115 120 125
 Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly
 130 135 140
 Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln
 145 150 155 160
 His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly
 165 170 175
 Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu
 180 185 190

Ala Phe Leu Ser Gly Tyr Val Thr Leu Ala Ala Gln Leu Ala
 195 200 205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
 210 215 220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
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Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
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Gly

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atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99
 Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly
 15 20 25 30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147
 Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg
 35 40 45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195
 Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
 50 55 60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243
 Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
 65 70 75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291
 Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
 80 85 90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339
 Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95 100 105 110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387
 Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
 115 120 125

gct ggg gag ctg tac c cg g aaa cct cgc agc cgc tcc c cag tcc 435
 Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser
 130 135 140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483
 Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser
 145 150 155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531
 Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro
 160 165 170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579
 Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
 175 180 185 190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627
 Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
 195 200 205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675
 Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
 210 215 220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723
 Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
 225 230 235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771
 Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
 240 245 250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acaggagacc 820
 Thr Asp Gly
 255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttatatt atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttgaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggtttotca 1300

gggatgccaa ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480

<210> 57
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 57
 Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln
 1 5 10 15
 Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
 20 25 30
 Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
 35 40 45
 Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
 50 55 60
 Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
 65 70 75 80
 Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
 85 90 95
 Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
 100 105

<210> 58
 <211> 1496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (9)..(329)

<400> 58
 ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac 50
 Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
 1 5 10
 atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98
 ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
 15 20 25 30
 gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146
 Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
 35 40 45
 gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194
 Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
 50 55 60
 cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242

Arg Phe Arg Leu Thr Glu Ser Thr Asn Gln Arg Val L Trp Trp
65 70 75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290
Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met
80 85 90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgcctc 339
Arg His Leu Lys Ser Phe Glu Ala Lys Lys Leu Val
95 100 105

tttgtatgac ccttcctttt tacctcattt atttgggtact ttccccacac agtcctttat 399
ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459
caaaccattc agatcagcca ctgtctgacc ctggttctta aggacacatg acattagtcc 519
aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccga ggactcagtc 579
ctgcttcttt tgccctcagat gattttcctc tgtttttcac taaataagca aatgaaaact 639
ctctccatta ccttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699
acagagcagg cctgcctca ctgtctgctg gtcagttctg ggttcactta atggctttgt 759
gaatgtaa at aaggggcagg tcttggccct agaggattga gatgttttc tatacttag 819
aactattttt ggataaatta tatattttcc ttcctagtag aagtgttact gcctgtaact 879
agctcaaaat accaatgcag tttctgcatt ctgggttttg ttttctttt ttttttttt 939
ttttttgagt tttgctcttg tcgcccaggc tggagtgcaa tggcgtgatc tcagctcact 999
ggcaacatct gcctcccggg ttcaaatgat tctcctgcct cagtctcctg agtagctggg 1059
attacagtg cccgccacca cgctcagcta atttttgtat ttttagtaga gatgggggtt 1119
taccatgttg gccaggctgg tcttagactc ctgacctcag ttgatccacc tgcctcagcc 1179
tctgcattca gtttattcac atattttttg taactcccat ggcagctcct aggatttcag 1239
cggctctgtg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299
gcagagttct tttggatacc tgcttttcat cccacagggc cttagagtca gaggttaagg 1359
agcaacagag ctagaatggg gcaatgcact cttaccctcc ttctcaactt ttatttaagc 1419
tgtgctaaat gttttcttca agggaaccag atttagttct ttacagaatt ttccagtga 1479
ataaaacatg ttgtaat 1496

<210> 59
<211> 272
<212> PRT
<213> Homo sapiens

<400> 59

Met Met Ile His Glu Phe Gln Ser Ser His Arg Asp Phe Phe Gly
 1 5 10 15
 Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp
 20 25 30
 Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met
 35 40 45
 Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
 50 55 60
 Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
 65 70 75 80
 Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
 85 90 95
 Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
 100 105 110
 Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
 115 120 125
 Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
 130 135 140
 Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
 145 150 155 160
 His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro
 165 170 175
 Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val
 180 185 190
 Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr
 195 200 205
 Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu
 210 215 220
 Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln
 225 230 235 240
 Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu
 245 250 255
 Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
 260 265 270

<210> 60
 <211> 1916
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (117).. (932)

<400> 60

atggtaacgg ctcggaagcc taggaggctg ggccggaggg aggcggagga accggtgttc 60

gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119
 Met
 1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167
 Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro
 5 10 15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215
 Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val
 20 25 30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263
 Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met
 35 40 45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311
 Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile
 50 55 60 65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359
 Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly
 70 75 80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407
 Met Leu Lys Val -Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu
 85 90 95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455
 Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr
 100 105 110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503
 Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val
 115 120 125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551
 Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
 130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599
 Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
 150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647
 Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
 165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695
 Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu
 180 185 190

atc aga atg aat gac gga gga ctt tac cat gag gct gac acc tac	743
Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr	
195 200 205	
atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg	791
Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met	
210 215 220 225	
cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat	839
His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr	
230 235 240	
tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga	887
Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg	
245 250 255	
att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa	932
Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu	
260 265 270	
taaaatgtga tacaacatat actcactatg gaatctgact ggacacottg gctattttgta	992
aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct	1052
taaaggaaaa aaaaataaag atcggtacag gcagggtttca ctcaactgct atttgtactg	1112
tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct	1172
aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagttagca	1232
cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca	1292
aatcccaatg ccttggtgact ttcataggat tcctgatcat gcatgttgat gtactggctc	1352
ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac	1412
gaaattagtc tcatagtgtg gtgaacttca accccaaaat tttaaaaatg tatttcccc	1472
cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaa	1532
aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct	1592
gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttggt gattcagatg	1652
tcttgggtccc tgaatagtcc tagattactt attttgagaa ttgattgtta aaaattacag	1712
ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc	1772
tctgaaaatt ttattagttt attcttgttg agaataccaa gaaaatgtgt atttgcccat	1832
tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtctt ttttaagagg	1892
agaataaaca ataaggaatt actg	1916

<210> 61
 <211> 219
 <212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Ser
1 5 10 15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp
20 25 30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
35 40 45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
50 55 60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
65 70 75 80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
85 90 95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
100 105 110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
115 120 125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
130 135 140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
145 150 155 160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
165 170 175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
180 185 190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
195 200 205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
210 215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49).. (705)

<400> 62

gttttctggt ttgtctctag tgtttgggtt tcttcgcggc tgctcaag atg aac cga 57
Met Asn Arg

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac	105
Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp	
5 10 15	
tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att	153
Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile	
20 25 30 35	
tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag	201
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys	
40 45 50	
atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga	249
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg	
55 60 65	
gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc	297
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala	
70 75 80	
caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg	345
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu	
85 90 95	
aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa	393
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu	
100 105 110 115	
atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta	441
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu	
120 125 130	
caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa	489
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu	
135 140 145	
gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta	537
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu	
150 155 160	
gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac	585
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp	
165 170 175	
agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt	633
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly	
180 185 190 195	
gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt	681
Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe	
200 205 210	
gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta	735
Gly Leu Pro Gln Ile Pro Ala Ser	
215	

aaacaaacac atattatg actaggaaat atttatcttt ccaaatttg ataacagat 795
 ttaggtttct ttccctttctt tgaaggaaag ttttaattaca ttgctctttt atttttcca 855
 ttaagagact cattgcttgg gaaatgcttt ctctgtacta aaatttgatt cctttttttt 915
 cttatgaaaa acgaactcag tttaaaagta ttttagctc gtatgacttg tttcattca 975
 ttaataataa tttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035
 ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095
 ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg 1155
 cctttttgat gggttttggt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa 1215
 tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcaagtatta 1275
 catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335
 tatactcaat aaatattttt caaaagg 1362

<210> 63
 <211> 622
 <212> PRT
 <213> Homo sapiens

<400> 63

Met	Ala	Asp	Gly	Pro	Asp	Glu	Tyr	Asp	Thr	Glu	Ala	Gly	Cys	Val	Pro
1				5					10					15	
Leu	Leu	His	Pro	Glu	Glu	Ile	Lys	Pro	Gln	Ser	His	Tyr	Asn	His	Gly
		20					25						30		
Tyr	Gly	Glu	Pro	Leu	Gly	Arg	Lys	Thr	His	Ile	Asp	Asp	Tyr	Ser	Thr
		35					40					45			
Trp	Asp	Ile	Val	Lys	Ala	Thr	Gln	Tyr	Gly	Ile	Tyr	Glu	Arg	Cys	Arg
	50					55					60				
Glu	Leu	Val	Glu	Ala	Gly	Tyr	Asp	Val	Arg	Gln	Pro	Asp	Lys	Glu	Asn
65					70					75					80
Val	Thr	Leu	Leu	His	Trp	Ala	Ala	Ile	Asn	Asn	Arg	Ile	Asp	Leu	Val
				85					90					95	
Lys	Tyr	Tyr	Ile	Ser	Lys	Gly	Ala	Ile	Val	Asp	Gln	Leu	Gly	Gly	Asp
			100					105					110		
Leu	Asn	Ser	Thr	Pro	Leu	His	Trp	Ala	Thr	Arg	Gln	Gly	His	Leu	Ser
		115					120					125			
Met	Val	Val	Gln	Leu	Met	Lys	Tyr	Gly	Ala	Asp	Pro	Ser	Leu	Ile	Asp
130						135					140				
Gly	Glu	Gly	Cys	Ser	Cys	Ile	His	Leu	Ala	Ala	Gln	Phe	Gly	His	Thr
145					150					155					160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met
 165 170 175
 Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His
 180 185 190
 Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn
 195 200 205
 Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu
 210 215 220
 Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn
 225 230 235 240
 Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys
 245 250 255
 Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln
 260 265 270
 Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp
 275 280 285
 Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile
 290 295 300
 Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile
 305 310 315 320
 Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser
 325 330 335
 Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile
 340 345 350
 Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe
 355 360 365
 Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn
 370 375 380
 Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
 385 390 395 400
 Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
 405 410 415
 Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
 420 425 430
 Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
 435 440 445
 Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
 450 455 460

Gly Ala Gly Asn His Tyr Phe Met Gly Tyr Leu Phe Leu Leu
 465 470 475 480
 Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
 485 490 495
 His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
 500 505 510
 Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
 515 520 525
 Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
 530 535 540
 Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
 545 550 555 560
 Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
 565 570 575
 Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
 580 585 590
 Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
 595 600 605
 Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
 610 615 620

<210> 64
 <211> 2948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14).. (1879)

<400> 64
 atttaacacc aag atg gcg gac ggc ccg gat gag tac gat acc gaa gcg 49
 Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala
 1 5 10
 ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97
 Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
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 tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145
 Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp
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 Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr
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Asp	Lys	Glu	Asn	Val	Thr	Leu	Leu	His	Trp	Ala	Ala	Ile	Asn	Asn	Arg	
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Ile	Asp	Leu	Val	Lys	Tyr	Tyr	Ile	Ser	Lys	Gly	Ala	Ile	Val	Asp	Gln	
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Leu	Gly	Gly	Asp	Leu	Asn	Ser	Thr	Pro	Leu	His	Trp	Ala	Thr	Arg	Gln	
	110					115					120					
ggc	cat	cta	tcc	atg	gtt	gtg	caa	cta	atg	aaa	tat	ggt	gca	gat	cct	433
Gly	His	Leu	Ser	Met	Val	Val	Gln	Leu	Met	Lys	Tyr	Gly	Ala	Asp	Pro	
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tca	tta	att	gat	gga	gaa	gga	tgt	agc	tgt	att	cat	ctg	gct	gct	cag	481
Ser	Leu	Ile	Asp	Gly	Glu	Gly	Cys	Ser	Cys	Ile	His	Leu	Ala	Ala	Gln	
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Phe	Gly	His	Thr	Ser	Ile	Val	Ala	Tyr	Leu	Ile	Ala	Lys	Gly	Gln	Asp	
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Val	Asp	Met	Met	Asp	Gln	Asn	Gly	Met	Thr	Pro	Leu	Met	Trp	Ala	Ala	
		175					180					185				
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Tyr	Arg	Thr	His	Ser	Val	Asp	Pro	Thr	Arg	Leu	Leu	Leu	Thr	Phe	Asn	
	190					195					200					
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Val	Ser	Val	Asn	Leu	Gly	Asp	Lys	Tyr	His	Lys	Asn	Thr	Ala	Leu	His	
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tgg	gca	gtg	cta	gca	ggg	aat	acc	aca	gtc	att	agc	ctt	ctt	ctg	gaa	721
Trp	Ala	Val	Leu	Ala	Gly	Asn	Thr	Thr	Val	Ile	Ser	Leu	Leu	Leu	Glu	
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gct	gga	gct	aat	gtt	gat	gcc	cag	aat	atc	aag	ggc	gaa	tca	gcg	ctt	769
Ala	Gly	Ala	Asn	Val	Asp	Ala	Gln	Asn	Ile	Lys	Gly	Glu	Ser	Ala	Leu	
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Asp	Leu	Ala	Lys	Gln	Arg	Lys	Asn	Val	Trp	Met	Ile	Asn	His	Leu	Gln	
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Glu	Ala	Arg	Gln	Ala	Lys	Gly	Tyr	Asp	Asn	Pro	Ser	Phe	Leu	Arg	Lys	
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Leu	Lys	Ala	Asp	Lys	Glu	Phe	Arg	Gln	Lys	Val	Met	Leu	Gly	Thr	Pro	
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Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val	
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Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu	
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ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg	1105
Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp	
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Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro	
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Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp	
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Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys	
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Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe	
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Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly	
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Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val	
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Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser	
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Tyr Trp Gly Leu His Cys Glu Thr Thr Lys Asp Gly Phe Trp	
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aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg	1585
Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met	
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 Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg
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 Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile
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gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc 1825
 Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr
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 Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln
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Arg	Lys	Thr	His	Ile	Asp	Asp	Tyr	Ser	Thr	Trp	Asp	Ile	Val	Lys	Ala
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Tyr	Asp	Val	Arg	Gln	Pro	Asp	Lys	Glu	Asn	Val	Thr	Leu	Leu	His	Trp
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Ala	Ala	Ile	Asn	Asn	Arg	Ile	Asp	Leu	Val	Lys	Tyr	Tyr	Ile	Ser	Lys
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Gly	Ala	Ile	Val	Asp	Gln	Leu	Gly	Gly	Asp	Leu	Asn	Ser	Thr	Pro	Leu
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Lys	Tyr	Gly	Ala	Asp	Pro	Ser	Leu	Ile	Asp	Gly	Glu	Gly	Cys	Ser	Cys
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Ile	His	Leu	Ala	Ala	Gln	Phe	Gly	His	Thr	Ser	Ile	Val	Ala	Tyr	Leu
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Ile	Ala	Lys	Gly	Gln	Asp	Val	Asp	Met	Met	Asp	Gln	Asn	Gly	Met	Thr
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Pro	Leu	Met	Trp	Ala	Ala	Tyr	Arg	Thr	His	Ser	Val	Asp	Pro	Thr	Arg
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Leu	Leu	Leu	Thr	Phe	Asn	Val	Ser	Val	Asn	Leu	Gly	Asp	Lys	Tyr	His
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Lys	Asn	Thr	Ala	Leu	His	Trp	Ala	Val	Leu	Ala	Gly	Asn	Thr	Thr	Val
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Lys	Gly	Glu	Ser	Ala	Leu	Asp	Leu	Ala	Lys	Gln	Arg	Lys	Asn	Val	Trp

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 Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
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 Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
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 450 455 460
 His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg
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 485 490 495
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Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp
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acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212
Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro
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caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260
Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr
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His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr
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Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val
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Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile
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Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile
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Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala	
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Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu	
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Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr	
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Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu	
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Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn	
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Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu	
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Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu	
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 Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly
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 Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp
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 tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823
 acagttccat ttttaagggt taagggtgta ttttcaagaa aaggcagaac aaataatgca 2883
 aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943
 attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003
 tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag 3063
 tagaatttca tccccaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123
 tttagaaaaa attttctttt tgttaaagt gatgcactga tcaatttttg tcacagcatt 3183
 ttcatacctt catgggtggac tactagtcac tgcttccata aatattgttt acagggtgag 3243
 atttggttta ttcattctaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303

ctgtgagagg gaatgggg ggagatgtgg gggaatgggtg gtcagactg gacagatcc 3363
 tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423
 gtgtctgtgt tagtggtttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483
 gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543
 caagttcact gcatgtctga tgcttggtaa aactagtctt ccctgtaaaa tgcagattac 3603
 aggtattaaa gcaatctagt ggtatacccg ccccttgccct tagtaagagg agcagtgaaa 3663
 tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723
 ataagtcaca catcaaaaaa agattaccct tagtgtatgt gttttaatat tagaaaattg 3783
 gcatatgtac tttatttttg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843
 ccattttgtc atagaatgta aaaattggtt aactttacaa atgtcagcta gttttgacta 3903
 ctaattgggg gaaattttag ataattttta aattcaaagt tatttataaa atgctagaat 3963
 ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023
 aatacatttt tatcaacagt taaagactat ggtgggtttt tcagagtttg gctaagaatg 4083
 ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag 4143
 ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt 4203
 ttgtagtaac catctttag tacctgtgaa atctataact cagaaatggc cagatgggtca 4263
 ggagccagct atgcagcagt ataccatctg ttttaattatt ttgtaggtcc tgtgtgtgga 4323
 accaactata aaccagttc taaagtgtg tatgatgggtg aacctttggg aatagttctt 4383
 atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443
 tacttccttg gagttttttt tcattcatat tttgtttgtt tccaggaatt tatttgatat 4503
 taatgggcgt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatattc 4563
 tttatttata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa 4623
 aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg 4683
 taaaatatta atcagaataa atactgactc tt 4715

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1

5

10

15

Leu Val Ser Pro Asn Ser His Ser His Ala Val Val Ser Trp
 20 25 30
 Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
 35 40 45
 Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
 50 55 60
 Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
 65 70 75 80
 Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
 85 90 95
 Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
 100 105 110
 Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
 115 120 125
 Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
 130 135 140
 Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
 145 150 155 160
 Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
 165 170 175
 Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
 180 185 190
 Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
 195 200 205
 Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
 210 215 220
 Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
 225 230 235 240
 Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
 245 250 255
 Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
 260 265 270
 His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
 275 280 285
 Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
 290 295 300
 Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
 305 310 315 320
 Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
 340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
 355 360 365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
 370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
 385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
 405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
 420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
 435 440 445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
 450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
 465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
 485 490 495

Ser Cys

<210> 68
 <211> 1902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (22).. (1515)

<400> 68
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 Met Ala Arg Leu Glu Val Ile Glu Leu Pro 10
 1 5

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
 His Ser Pro Gln Asn Leu Val Ser Pro Asn Ser Ser His Ser His 25
 15 20

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
 Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile 40
 30 35

ctt tat tac atc gtg g ctg tct gaa aac aac tct cca t aag gtg	195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val	
45 50 55	
cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc	243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly	
60 65 70	
ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa	291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu	
75 80 85 90	
gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct	339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro	
95 100 105	
gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg	387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg	
110 115 120	
act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag	435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu	
125 130 135	
cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc	483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly	
140 145 150	
ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac	531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn	
155 160 165 170	
tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag	579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln	
175 180 185	
gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg	627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val	
190 195 200	
acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg	675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val	
205 210 215	
cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct	723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro	
220 225 230	
ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg	771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu	
235 240 245 250	
gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc	819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala	
255 260 265	
cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag	867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys	

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac	915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp	
285 290 295	
ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca	963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro	
300 305 310	
gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc	1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu	
315 320 325 330	
aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc	1059
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly	
335 340 345	
tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg	1107
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr	
350 355 360	
cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca	1155
His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser	
365 370 375	
tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc	1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly	
380 385 390	
act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac	1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp	
395 400 405 410	
ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc	1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg	
415 420 425	
tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc	1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile	
430 435 440	
tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta	1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu	
445 450 455	
cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca	1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala	
460 465 470	
aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc	1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser	
475 480 485 490	
cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat	1545
Gln Lys Leu Trp Glu Phe Ser Cys	
495	

aaagaattca tatcatc taatggcgac agtttttgtt tcttcctt ttttttttat 1605
 attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665
 gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725
 cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785
 aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845
 atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69
 <211> 498
 <212> PRT
 <213> Homo sapiens

<400> 69
 Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
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 Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
 20 25 30
 Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
 35 40 45
 Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
 50 55 60
 Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
 65 70 75 80
 Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
 85 90 95
 Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
 100 105 110
 Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
 115 120 125
 Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
 130 135 140
 Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
 145 150 155 160
 Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
 165 170 175
 Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
 180 185 190
 Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
 195 200 205

Gly Val Pro Thr Al~~o~~ Pro Gln Asn Val Gln Thr Glu~~o~~ Val Asn
 210 215 220
 Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
 225 230 235 240
 Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
 245 250 255
 Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
 260 265 270
 His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
 275 280 285
 Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
 290 295 300
 Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
 305 310 315 320
 Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
 325 330 335
 Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
 340 345 350
 Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
 355 360 365
 Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
 370 375 380
 Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
 385 390 395 400
 Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
 405 410 415
 Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
 420 425 430
 Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
 435 440 445
 Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
 450 455 460
 Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
 465 470 475 480
 Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
 485 490 495
 Ser Cys

<210> 70
 <211> 1902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (22).. (1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct	51
Met Ala Arg Leu Glu Val Ile Glu Leu Pro	10
cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac	99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His	25
gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att	147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile	40
ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg	195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val	55
cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc	243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly	70
ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa	291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu	90
gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct	339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro	105
gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg	387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg	120
act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag	435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu	135
cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc	483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly	150
ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac	531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn	170
tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag	579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln	185

gtg gcg gcg tac aac ggc ggt ctg ggc gtc ttc agc aca gca gtg	627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val	
190 195 200	
acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg	675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val	
205 210 215	
cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct	723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro	
220 225 230	
ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg	771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu	
235 240 245 250	
gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc	819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala	
255 260 265	
cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag	867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys	
270 275 280	
ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac	915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp	
285 290 295	
ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca	963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro	
300 305 310	
gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc	1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu	
315 320 325 330	
aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc	1059
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly	
335 340 345	
tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg	1107
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr	
350 355 360	
cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca	1155
His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser	
365 370 375	
tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc	1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly	
380 385 390	
act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac	1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp	
395 400 405 410	
ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc	1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg	

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
 Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
 430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta 1395
 Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu
 445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
 Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
 460 465 470

aac ctg gga agt ctg tgg ctg ctg agc ctg gtg tat tgg tgt tac agc 1491
 Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
 475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttggta gttttactgt aattttctat 1545
 Gln Lys Leu Trp Glu Phe Ser Cys
 495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaactt tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcaggatg gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg 1845

atttcctagg agttgggttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
 1 5 10 15

Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
 20 25 30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
 35 40 45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
 50 55 60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
 65 70 75 80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
 85 90 95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
 100 105 110
 Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
 115 120 125
 Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
 130 135 140
 Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
 145 150 155 160
 Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
 165 170 175
 Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
 180 185 190
 Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
 195 200 205
 Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
 210 215 220
 Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
 225 230 235 240
 Gln Trp Ile Gln Arg
 245

<210> 72
 <211> 1551
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (127).. (861)

<400> 72
 ggaagtcggc caccttctc cgtcccgcc gttagcccag ccaagcccag ccaagcccag 60
 ccaagccccg ccgatcgcg gcaccggagc cagccccgca gcgggtccc cctgtctgtc 120
 acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168
 Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser
 1 5 10
 atg cac tcc ctg cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216
 Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser
 15 20 25 30
 atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264
 Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile
 35 40 45

ctg acg ttc ttt gtg gct gcc atc ctc tgg ctg ctc tcc cac	312
Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His	
50 55 60	
cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg	360
Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg	
65 70 75	
ctc ggc cag ggc ccc gcc aac tgg tac aat gac acc tac ccc ctg tct	408
Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser	
80 85 90	
ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc	456
Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile	
95 100 105 110	
gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc	504
Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe	
115 120 125	
agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag	552
Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys	
130 135 140	
gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg	600
Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu	
145 150 155	
gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat	648
Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn	
160 165 170	
ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc	696
Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile	
175 180 185 190	
gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc	744
Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly	
195 200 205	
acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att	792
Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile	
210 215 220	
gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt	840
Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val	
225 230 235	
ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact	891
Leu Gly Gln Trp Ile Gln Arg	
240 245	
gtcagaaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc	951
ctagggtctg tgaacgaggc ctgtctcttc cctgggggttt ctttccatgg cctttatttc	1011
tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggtc	1071

ggcctcggct tcgctgga gttactccagg gtgaaggcag agtgggatt agaccagg 1131
 tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191
 tcaccgggca tagcctggaa gcccgaagtc tgttctgact ttgcctggct gtctccttga 1251
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 tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371
 tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431
 gcgattactt taaagctcac ctttttctt cccctctctg ttcgctgctg tcagcataat 1491
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<210> 73
 <211> 352
 <212> PRT
 <213> Homo sapiens

<400> 73
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 1 5 10 15
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
 20 25 30
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
 35 40 45
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
 50 55 60
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
 65 70 75 80
 Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
 85 90 95
 Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
 100 105 110
 Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
 115 120 125
 Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
 130 135 140
 Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
 145 150 155 160
 Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
 165 170 175
 Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
 180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
195 200 205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
210 215 220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225 230 235 240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
245 250 255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
290 295 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
340 345 350

<210> 74
<211> 2401
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (103).. (1158)

<400> 74
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tatccttggc gccacagtcg gccaccgggg ctgcgcccg tc atg gag agc gga 114
Met Glu Ser Gly
1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
25 30 35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata	306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile	
55 60 65	
gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg	354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val	
70 75 80	
gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag	402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys	
85 90 95 100	
atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc	450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile	
105 110 115	
att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag	498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu	
120 125 130	
gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg	546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val	
135 140 145	
gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag	594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln	
150 155 160	
tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa	642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys	
165 170 175 180	
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca	690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr	
185 190 195	
ggg gtt ggc gaa ctg gtc ctg gac aac aac tot gtc cgc ctg cag ccg	738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro	
200 205 210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc	786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser	
215 220 225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg	834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala	
230 235 240	
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg	882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg	
245 250 255 260	
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag	930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln	
265 270 275	

gag gag ttc cag gag ttc gag gcc cag ctg ctg agc cga gag aag cct 978
 Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
 280 285 290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026
 Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
 295 300 305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074
 Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
 310 315 320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122
 Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
 325 330 335 340

cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg 1168
 Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
 345 350

gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga 1228
 ggccctttgga ggagcagttg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288
 tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348
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 tcgcttctcc ttgtgttacc cctcccagc attaccattt gccctcacc tgcccttggg 2188
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ctttgtgcag gcgagga ggtgccctca ggggccgaca ctagtgtg scagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc

2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
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Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
195 200 205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
210 215 220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225 230 235 240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
245 250 255

85										95					100	
atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc	Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile	450														
	105 110 115															
att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag	Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu	498														
	120 125 130															
gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg	Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val	546														
	135 140 145															
gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag	Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln	594														
	150 155 160															
tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa	Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys	642														
	165 170 175 180															
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca	Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr	690														
	185 190 195															
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg	Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro	738														
	200 205 210															
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc	Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser	786														
	215 220 225															
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg	Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala	834														
	230 235 240															
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg	Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg	882														
	245 250 255 260															
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag	Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln	930														
	265 270 275															
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct	Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro	978														
	280 285 290															
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc	Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser	1026														
	295 300 305															
ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc	Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr	1074														
	310 315 320															

gag tgc tac cgc gc g cca gag ccc aag aag tgc cct tgc aga 1122
 Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Phe Cys Arg
 325 330 335 340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg 1168
 Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
 345 350

gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228
 ggccctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288
 tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348
 gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctggggagga tgccgtggcg 1408
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 tcgcttctcc ttgtgttacc cctcccagt attaccattt gccctcacc tgcccttggg 2188
 gagcctttta gtgcaagaca gatggggctg tttccccca cctctgagta gttggaggtc 2248
 acatacacag ctctttttt attgccctt tctgcctctg aatgttcac tctcgtcctc 2308
 ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368
 gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 77
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 77
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Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser
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 Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile
 35 40 45
 Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile
 50 55 60
 Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile
 65 70 75 80
 Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
 85 90 95
 Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser
 100 105 110
 Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
 115 120 125
 Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
 130 135 140
 Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
 145 150 155 160
 Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
 165 170 175
 Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
 180 185 190
 Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
 195 200 205
 Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
 210 215 220
 Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
 225 230 235 240
 Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
 245 250 255
 Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
 260 265 270
 Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
 275 280 285
 His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
 290 295 300
 Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
 305 310 315 320



Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp
 325 330 335
 Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe
 340 345 350
 Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
 355 360 365
 Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
 370 375 380
 Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
 385 390 395 400
 His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
 405 410 415
 Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu
 420 425 430
 Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
 435 440 445
 Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
 450 455 460
 Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
 465 470 475 480
 Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
 485 490 495
 Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
 500 505 510
 Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
 515 520 525
 Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
 530 535 540
 Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
 545 550 555 560
 Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
 565 570 575
 Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
 580 585 590
 Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
 595 600 605
 Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
 610 615 620

Tyr Thr Leu His Leu Thr Gly Ser Asp Val Ala Lys Hrp Met
 625 630 635 640
 Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
 645 650 655
 Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
 660 665 670
 Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
 675 680 685
 Gly Gln Gly Phe Lys Leu Val Lys Ser
 690 695

<210> 78
 <211> 3008
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (372).. (2462)

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 ggcgtagccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180
 ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240
 cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300
 ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360
 ttgctgggta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410
 Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu
 1 5 10
 tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458
 Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
 15 20 25
 cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506
 His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu
 30 35 40 45
 gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554
 Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
 50 55 60
 tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602
 Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile
 65 70 75

gcc agc ata ctc tat  tat ttt tca atg gaa gca gca  ata agt	650
Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser	
80 85 90	
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Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu	
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gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat	746
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr	
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ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag	794
Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu	
130 135 140	
aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt	842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val	
145 150 155	
gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg	890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu	
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Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met	
175 180 185	
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Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu	
190 195 200 205	
gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa	1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys	
210 215 220	
aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct	1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro	
225 230 235	
ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa	1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys	
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ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt	1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe	
255 260 265	
gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt	1226
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu	
270 275 280 285	
aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt	1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe	
290 295 300	
gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg	1322
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp	

gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His 320 325 330	1370
agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met 335 340 345	1418
cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu 350 355 360 365	1466
gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile 370 375 380	1514
ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His 385 390 395	1562
ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly 400 405 410	1610
tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro 415 420 425	1658
aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr 430 435 440 445	1706
ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu 450 455 460	1754
acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu 465 470 475	1802
cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro 480 485 490	1850
aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr 495 500 505	1898
gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu 510 515 520 525	1946
ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile 530 535 540	1994

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 Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg
 545 550 555

aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090
 Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys
 560 565 570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138
 Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr
 575 580 585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186
 Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
 590 595 600 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234
 Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
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tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282
 Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
 625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330
 His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
 640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378
 Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
 655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426
 Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
 670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac 2472
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 690 695

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		20						25					30		
Lys	Glu	Glu	Ser	Thr	Lys	Tyr	Leu	Leu	Leu	Thr	Ser	Ile	Val	Leu	Arg
	35						40					45			
Ile	Leu	Cys	Ser	Leu	Val	Glu	Arg	Ile	Ser	Gly	Tyr	Val	Arg	His	Arg
	50					55					60				
Pro	Thr	Leu	Leu	Thr	Thr	Val	Glu	Phe	Leu	Glu	Leu	Val	Gly	Phe	Ala
65					70					75					80
Ile	Ala	Ser	Thr	Thr	Met	Leu	Val	Glu	Lys	Ser	Leu	Ser	Val	Ile	Leu
				85					90					95	
Leu	Val	Val	Ala	Leu	Ala	Met	Leu	Ile	Ile	Asp	Leu	Arg	Met	Lys	Ser
			100					105					110		
Phe	Leu	Ala	Ile	Pro	Asn	Leu	Val	Ile	Phe	Ala	Val	Leu	Leu	Phe	Phe
	115						120					125			
Ser	Ser	Leu	Glu	Thr	Pro	Lys	Asn	Pro	Ile	Ala	Phe	Ala	Cys	Phe	Phe
	130					135					140				
Ile	Cys	Leu	Ile	Thr	Asp	Pro	Phe	Leu	Asp	Ile	Tyr	Phe	Ser	Gly	Leu
145					150					155					160
Ser	Val	Thr	Glu	Arg	Trp	Lys	Pro	Phe	Leu	Tyr	Arg	Gly	Arg	Ile	Cys
				165					170					175	
Arg	Arg	Leu	Ser	Val	Val	Phe	Ala	Gly	Met	Ile	Glu	Leu	Thr	Phe	Phe
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Ile	Leu	Ser	Ala	Phe	Lys	Leu	Arg	Asp	Thr	His	Leu	Trp	Tyr	Phe	Val
	195						200					205			
Ile	Pro	Gly	Phe	Ser	Ile	Phe	Gly	Ile	Phe	Trp	Met	Ile	Cys	His	Ile
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Ile	Phe	Leu	Leu	Thr	Leu	Trp	Gly	Phe	His	Thr	Lys	Leu	Asn	Asp	Cys
225					230					235					240
His	Lys	Val	Tyr	Phe	Thr	His	Arg	Thr	Asp	Tyr	Asn	Ser	Leu	Asp	Arg
				245					250					255	
Ile	Met	Ala	Ser	Lys	Gly	Met	Arg	His	Phe	Cys	Leu	Ile	Ser	Glu	Gln
		260						265					270		

Leu Val Phe Phe Ser Leu Ala Thr Ala Ile Leu Gly Val Ser
 275 280 285
 Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
 290 295 300
 Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
 305 310 315 320
 Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe
 325 330 335
 Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
 340 345 350
 Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe
 355 360 365
 Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser
 370 375 380
 Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu
 385 390 395 400
 Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr
 405 410 415
 Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp
 420 425 430
 Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly
 435 440 445
 Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr
 450 455 460
 Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val
 465 470 475 480
 Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro
 485 490 495
 Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
 500 505 510
 Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
 515 520 525
 Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro
 530 535 540
 Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile
 545 550 555 560
 Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu
 565 570 575
 Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met

585

Val Lys Ser
610

<400> 80

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ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgtctt cctccttttt 180
ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240
cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300
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aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600
cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652
Met Glu Ala Ala Ser Leu Ser Leu
1 5
tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc ctatgt ttt ctt gat 700
Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp
10 15 20
aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748
Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu
25 30 35 40
ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796
Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg
45 50 55
att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844
Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu
60 65 70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val 75 80 85	892
gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu 90 95 100	940
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ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe 140 145 150	1084
ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro 155 160 165	1132
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aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg 250 255 260	1420
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Leu Ser Met Phe Leu Val Leu Pro Leu Glu Ser Met A is Gly	
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Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr	
315 320 325	
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Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr	
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Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly	
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Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr	
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Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His	
380 385 390	
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Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg	
395 400 405	
cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga	1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly	
410 415 420	
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Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile	
425 430 435 440	
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Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile	
445 450 455	
gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa	2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys	
460 465 470	
att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca	2092
Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr	
475 480 485	
gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa	2140
Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys	
490 495 500	
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Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr	
505 510 515 520	
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Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp	
525 530 535	

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 Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His
 540 545 550

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 Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala
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 605 610

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 Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln
 50 55 60

Val Ser Arg Val Gl⁷⁰e Ser Leu Gln Leu Phe Lys Lys⁷⁵ Asn Ser⁸⁰
 Ser Val Leu Ser Phe⁸⁵ Glu Ile Lys Asn Met⁹⁰ Ser Lys Lys Thr Asn⁹⁵ Leu
 Ile Val Asp Ser¹⁰⁰ Arg Glu Leu Gly Tyr¹⁰⁵ Leu Asn Lys Met Asp¹¹⁰ Leu Pro
 Tyr Arg Cys Met Val Arg Phe Gly¹²⁰ Glu Tyr Gln Phe Leu¹²⁵ Met Glu Lys
 Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser
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 tcctgcgccc agtctcctcg attcccctcg ctctgagccg ggagagccga acagctgaag 240
 agagttcact gactccccag cccaggtgg gccttggtgca catc atg acc agt ttt 296
 Met Thr Ser Phe
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 gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344
 Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val
 5 10 15 20
 tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392
 Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe
 25 30 35
 aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440
 Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn
 40 45 50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt	488
Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val	
55 60 65	
cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc	536
Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser	
70 75 80	
ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc	584
Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser	
85 90 95 100	
aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg	632
Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met	
105 110 115	
gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag	680
Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu	
120 125 130	
tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc	728
Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu	
135 140 145	
ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc	776
Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly	
150 155 160	
act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat	824
Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Pro Thr Glu Met Asp	
165 170 175 180	
gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa	876
Glu Asn Glu Ser	
gagctctgta gatgctgtat agacactaaa taagagtga ttagggtagt atattatagt 936	
catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996	
ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat ttttaactgct 1056	
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gaataggttc taggctagtg tctgcgcgtc actgtggttt tagcatggga ggacttattt 1356	
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taagatgaca gttctctttg tctatattca gcatctaaga caaatattta aacattttaa 1476	
agaaccactg tgttaagttt aggattatct acttaccaaa ttagaagttt gacttttatg 1536	

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270
 Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
 275 280 285
 Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
 290 295 300
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
 305 310 315 320
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
 325 330 335
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
 340 345 350
 Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
 355 360 365
 Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
 370 375 380
 Val Glu Ser Pro Val Gln Lys Val
 385 390

<210> 84
 <211> 1898
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (119).. (1294)

<400> 84
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 atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60

tac ctg gag acc ggt ggc ctc tgc ttt ccc ctg gtg aat gct tgt	358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys	
65 70 75 80	
gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc	406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro	
85 90 95	
cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg	454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu	
100 105 110	
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg	502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val	
115 120 125	
ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca	550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser	
130 135 140	
ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga	598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg	
145 150 155 160	
gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag	646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln	
165 170 175	
ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc	694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser	
180 185 190	
aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc	742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser	
195 200 205	
ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg	790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met	
210 215 220	
ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac	838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr	
225 230 235 240	
ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc	886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser	
245 250 255	
agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc	934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	
260 265 270	
ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc	982
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr	
275 280 285	
cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc	1030

Arg Phe Met Gly Ar s Ser Glu Phe Ala Ala His Ala Leu Leu
 290 295 300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
 305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
 325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
 340 345 350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222
 Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
 355 360 365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270
 Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
 370 375 380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324
 Val Glu Ser Pro Val Gln Lys Val
 385 390

gaaataggac cctccaccca tccccttctg ctgtaacctc tgaggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agtttattct 1504

gagccccggg ggtagacagt cctcagtgag gggttttggg gagtttgggg tcaagagagc 1564

ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctagctgtgc 1624

tctgccacct tccagactca ctcccctctg caaatacctg catttcttac cctggtgaga 1684

aaagcacaag cgggtgtaggc tccaatgctg ctttcccagg aggggtgaaga tgggtgctgtg 1744

ctgaggaaag gggatgcaga gccctgccca gcaccaccac ctctatgct cctggatccc 1804

taggctctgt tccatgagcc tgttcaggt tttgtactt tagaaatgta actttttgct 1864

cttataattt tattttatta aattaaatta ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270
 Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
 275 280 285
 Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
 290 295 300
 Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
 305 310 315 320
 Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
 325 330 335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
 340 345 350
 Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
 355 360 365
 Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
 370 375 380
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
 385 390 395 400
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
 405 410 415
 Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
 420 425 430

<210> 86
 <211> 2018
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (119)..(1414)

<400> 86
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 atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95

cga aca gag gcg gca g acc acc ccg atg tgg cag gcc c aag ctg Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu	454
100 105 110	
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val	502
115 120 125	
ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser	550
130 135 140	
ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg	598
145 150 155 160	
gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln	646
165 170 175	
ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser	694
180 185 190	
aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser	742
195 200 205	
ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met	790
210 215 220	
ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr	838
225 230 235 240	
ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser	886
245 250 255	
agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	934
260 265 270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	982
275 280 285	
cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	1030
290 295 300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	1078
305 310 315 320	
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	1126

325

330

335

ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag 1174
 Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
 340 345 350

ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc 1222
 Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
 355 360 365

atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt 1270
 Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
 370 375 380

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
 385 390 395 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
 405 410 415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414
 Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
 420 425 430

tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg 1474

ctgtaacctc tgaggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca 1534

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caaatacctg catttcttac cctggtgaga aaagcacaag cgggtgtaggc tccaatgctg 1834

ctttcccagg aggggtgaaga tggtgctgtg ctgaggaaag gggatgcaga gccctgcccc 1894

gcaccaccac ctccatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt 1954

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ctgc 2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

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 20 25 30
 Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His
 35 40 45
 Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser
 50 55 60
 Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys
 65 70 75 80
 Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val
 85 90 95
 Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe
 100 105 110
 Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala
 115 120 125
 Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu
 130 135 140
 Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser
 145 150 155 160
 Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu
 165 170 175
 Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile
 180 185 190
 Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg
 195 200 205
 Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu
 210 215 220
 Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala
 225 230 235

<210> 88
 <211> 2717
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (111).. (815)

<400> 88
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aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116
 Met Gly
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atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly 5 10 15	164
aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser 20 25 30	212
aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn 35 40 45 50	260
aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu 55 60 65	308
gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val 70 75 80	356
ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn 85 90 95	404
ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu 100 105 110	452
atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn 115 120 125 130	500
ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp 135 140 145	548
act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn 150 155 160	596
agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn 165 170 175	644
ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala 180 185 190	692
tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe 195 200 205 210	740
cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg 215 220 225	788
aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat	835

gtggctggct cttgttttgt aaaccaaagt attaatcttc acttgagaaa gcagtttcta 895
ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955
taaatttctg caggacagcc tataaaattg tggactttt tgatgtttca gtaaacttga 1015
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aaatggcccc aggagatctg atcacacttc ctcttgaggc acctctcatg gatgttgcaa 1255
taagcattcg ggtactatca cccagaaata tgaattgcc aatagaaca tttagcatgt 1315
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accagtc aa atgtattttc tgctgaaatc tgcatatttg gaggcatttc ccaccaccga 1435
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
 50 55 60
 Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65 70 75 80
 Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
 85 90 95
 Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
 100 105 110
 Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
 115 120 125
 Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
 130 135 140
 Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
 145 150 155 160
 Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
 165 170 175
 Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
 180 185 190
 Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
 195 200 205
 Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
 210 215 220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Asn Asn
 225 230 235 240

Gln Tyr Glu Ile Val
 245

<210> 90
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 <212> DNA
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 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
 1 5 10 15
 ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155
 Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
 20 25 30
 gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203
 Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
 35 40 45
 tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251
 Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
 50 55 60
 att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299
 Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
 65 70 75 80
 gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347
 Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
 85 90 95
 ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395
 Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
 100 105 110
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 Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
 115 120 125
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 Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
 130 135 140
 gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539
 Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
 145 150 155 160

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Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser	
165 170 175	
tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta	635
Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val	
180 185 190	
aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa	683
Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu	
195 200 205	
atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg	731
Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu	
210 215 220	
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Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn	
225 230 235 240	
cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc tctaccttta	834
Gln Tyr Glu Ile Val	
245	
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tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga	954
cctaaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca	1014
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Arg	Val	Pro	Met	Gly	Pro	Gly	Asp	Lys	Arg	Cys	Lys	Leu	Leu	Gly			
10				15						20				25			
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Ile	Gly	Ile	Leu	Val	Leu	Leu	Ile	Ile	Val	Ile	Leu	Gly	Val	Pro	Leu		
				30					35					40			
att	atc	ttc	acc	atc	aag	gcc	aac	agc	gag	gcc	tgc	cgg	gac	ggc	ctt	196	
Ile	Ile	Phe	Thr	Ile	Lys	Ala	Asn	Ser	Glu	Ala	Cys	Arg	Asp	Gly	Leu		
			45					50					55				
cgg	gca	gtg	atg	gag	tgt	cgc	aat	gtc	acc	cat	ctc	ctg	caa	caa	gag	244	
Arg	Ala	Val	Met	Glu	Cys	Arg	Asn	Val	Thr	His	Leu	Leu	Gln	Gln	Glu		
		60					65					70					
ctg	acc	gag	gcc	cag	aag	ggc	ttt	cag	gat	gtg	gag	gcc	cag	gct	gcc	292	
Leu	Thr	Glu	Ala	Gln	Lys	Gly	Phe	Gln	Asp	Val	Glu	Ala	Gln	Ala	Ala		
	75					80					85						
acc	tgc	aac	cac	act	gtg	atg	gcc	cta	atg	gct	tcc	ctg	gat	gca	gag	340	
Thr	Cys	Asn	His	Thr	Val	Met	Ala	Leu	Met	Ala	Ser	Leu	Asp	Ala	Glu		
	90				95				100						105		
aag	gcc	caa	gga	caa	aag	aaa	gtg	gag	gag	ctt	gag	gga	gag	atc	act	388	
Lys	Ala	Gln	Gly	Gln	Lys	Lys	Val	Glu	Glu	Leu	Glu	Gly	Glu	Ile	Thr		
			110					115					120				
aca	tta	aac	cat	aag	ctt	cag	gac	gcg	tct	gca	gag	gtg	gag	cga	ctg	436	
Thr	Leu	Asn	His	Lys	Leu	Gln	Asp	Ala	Ser	Ala	Glu	Val	Glu	Arg	Leu		
			125				130						135				
aga	aga	gaa	aac	cag	gtc	tta	agc	gtg	aga	atc	gcg	gac	aag	aag	tac	484	
Arg	Arg	Glu	Asn	Gln	Val	Leu	Ser	Val	Arg	Ile	Ala	Asp	Lys	Lys	Tyr		
		140					145					150					
tac	ccc	agc	tcc	cag	gac	tcc	agc	tcc	gct	gcg	gcg	ccc	cag	ctg	ctg	532	
Tyr	Pro	Ser	Ser	Gln	Asp	Ser	Ser	Ser	Ala	Ala	Ala	Pro	Gln	Leu	Leu		
	155					160					165						
att	gtg	ctg	ctg	ggc	ctc	agc	gct	ctg	ctg	cag	tgagatccca	ggaagctggc	585				
Ile	Val	Leu	Leu	Gly	Leu	Ser	Ala	Leu	Leu	Gln							
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<210> 93
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 93

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			20					25						30	
Glu	Ala	Trp	Lys	Arg	Phe	Val	Thr	Ala	Ala	Glu	Leu	Pro	Arg	Asp	Glu
		35					40					45			
Ala	Asp	Ala	Leu	Tyr	Glu	Ala	Leu	Lys	Lys	Leu	Arg	Thr	Tyr	Ala	Ala
	50					55					60				
Ile	Glu	Asp	Glu	Tyr	Val	Gln	Gln	Lys	Asp	Glu	Gln	Phe	Arg	Glu	Trp
65					70					75					80
Phe	Leu	Lys	Glu	Phe	Pro	Gln	Val	Lys	Arg	Lys	Ile	Gln	Glu	Ser	Ile
				85					90					95	
Glu	Lys	Leu	Arg	Ala	Leu	Ala	Asn	Gly	Ile	Glu	Glu	Val	His	Arg	Gly
			100					105					110		
Cys	Thr	Ile	Ser	Asn	Val	Val	Ser	Ser	Ser	Thr	Gly	Ala	Ala	Ser	Gly
		115					120					125			
Ile	Met	Ser	Leu	Ala	Gly	Leu	Val	Leu	Ala	Pro	Phe	Thr	Ala	Gly	Thr
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Ser	Leu	Ala	Leu	Thr	Ala	Ala	Gly	Val	Gly	Leu	Gly	Ala	Ala	Ser	Ala
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Val	Thr	Gly	Ile	Thr	Thr	Ser	Ile	Val	Glu	His	Ser	Tyr	Thr	Ser	Ser
				165					170					175	
Ala	Glu	Ala	Glu	Ala	Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ile	Asp	Arg	Leu
			180					185					190		
Lys	Val	Phe	Lys	Glu	Val	Met	Arg	Asp	Ile	Thr	Pro	Asn	Leu	Leu	Ser
		195					200					205			
Leu	Leu	Asn	Asn	Tyr	Tyr	Glu	Ala	Thr	Gln	Thr	Ile	Gly	Ser	Glu	Ile
	210					215					220				
Arg	Ala	Ile	Arg	Gln	Ala	Arg	Ala	Arg	Ala	Arg	Leu	Pro	Val	Thr	Thr
225					230					235					240
Trp	Arg	Ile	Ser	Ala	Gly	Ser	Gly	Gly	Gln	Ala	Glu	Arg	Thr	Ile	Ala
				245					250					255	
Gly	Thr	Thr	Arg	Ala	Val	Ser	Arg	Gly	Ala	Arg	Ile	Leu	Ser	Ala	Thr
			260					265					270		
Thr	Ser	Gly	Ile	Phe	Leu	Ala	Leu	Asp	Val	Val	Asn	Leu	Val	Tyr	Glu

275

280

285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
 290 295 300

Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
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Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His
 325 330

<210> 94

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175).. (1167)

<400> 94

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tcagtgactg gagagctcca aggaaagtct ctcaagtacc tggctgctgg cacc atg 177
Met
1gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225
Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg
5 10 15gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273
Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu
20 25 30gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321
Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala
35 40 45gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369
Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile
50 55 60 65gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt 417
Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe
70 75 80ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa 465
Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu
85 90 95aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc 513
Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys
100 105 110

acc atc tcc aac gt tcc agc tcc act ggc gct gcc ggc atc	561
Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile	
115 120 125	
atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt	609
Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser	
130 135 140 145	
ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg	657
Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val	
150 155 160	
act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca	705
Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala	
165 170 175	
gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag	753
Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys	
180 185 190	
gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt	801
Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu	
195 200 205	
ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt	849
Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg	
210 215 220 225	
gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg	897
Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp	
230 235 240	
cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc	945
Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly	
245 250 255	
acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act	993
Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr	
260 265 270	
tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca	1041
Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser	
275 280 285	
aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg	1089
Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg	
290 295 300 305	
cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc	1137
Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile	
310 315 320	
tat cag cgt ctg aat cca tgc cat acc cac tgaccccgaga ccagtgcagc	1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His	
325 330	
cagcaggggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga	1247

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 cacctactca cc 2039

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 <211> 407
 <212> PRT
 <213> Homo sapiens

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 Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
 20 25 30
 Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
 35 40 45
 Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
 50 55 60
 Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
 65 70 75 80
 Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
 85 90 95
 His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
 100 105 110
 Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
 115 120 125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
 130 135 140
 Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
 145 150 155 160
 Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
 165 170 175
 Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
 180 185 190
 Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
 195 200 205
 Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
 210 215 220
 Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
 225 230 235 240
 Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
 245 250 255
 Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
 260 265 270
 Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
 275 280 285
 Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
 290 295 300
 Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
 305 310 315 320
 Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
 325 330 335
 Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
 340 345 350
 Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
 355 360 365
 Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
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 <211> 1409

<212> DNA
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<222> (181)..(1401)

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tttgccttgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180
atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228
Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
1 5 10 15
ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276
Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
20 25 30
tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324
Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
35 40 45
cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372
Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
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gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420
Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65 70 75 80
aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468
Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
85 90 95
cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516
His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
100 105 110
att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc 564
Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
115 120 125
tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc 612
Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
130 135 140
ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc 660
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145 150 155 160
ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act 708
Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
165 170 175

aaa gat tca gat aaa g aag gaa ttt ttt gag aag tta c cac aca	756
Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr	
180 185 190	
ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa	804
Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys	
195 200 205	
ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc	852
Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr	
210 215 220	
atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa	900
Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys	
225 230 235 240	
gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga	948
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg	
245 250 255	
gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg	996
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu	
260 265 270	
cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac	1044
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp	
275 280 285	
ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc	1092
Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly	
290 295 300	
aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta	1140
Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu	
305 310 315 320	
atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta	1188
Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu	
325 330 335	
gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca	1236
Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser	
340 345 350	
aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca	1284
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser	
355 360 365	
gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa	1332
Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu	
370 375 380	
aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt	1380
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe	
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Val Cys Lys Tyr Lys Leu Leu	

<210> 97
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 <212> PRT
 <213> Homo sapiens

<400> 97

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His	Ser	Tyr	Cys	His	Leu	Cys	Ile	Thr	Asp	Phe	Phe	Lys	Asn	Pro	Ser
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Gln	Lys	Gln	Leu	Arg	Gln	Glu	Thr	Phe	Cys	Cys	Pro	Gln	Cys	Arg	Ala
	50					55					60				
Pro	Phe	His	Met	Asp	Ser	Leu	Arg	Pro	Asn	Lys	Gln	Leu	Gly	Ser	Leu
65					70					75					80
Ile	Glu	Ala	Leu	Lys	Glu	Thr	Asp	Gln	Glu	Met	Ser	Cys	Glu	Glu	His
				85					90					95	
Gly	Glu	Gln	Phe	His	Leu	Phe	Cys	Glu	Asp	Glu	Gly	Gln	Leu	Ile	Cys
			100					105					110		
Trp	Arg	Cys	Glu	Arg	Ala	Pro	Gln	His	Lys	Gly	His	Thr	Thr	Ala	Leu
		115					120					125			
Val	Glu	Asp	Val	Cys	Gln	Gly	Tyr	Lys	Glu	Lys	Leu	Gln	Glu	Ala	Val
	130					135					140				
Thr	Lys	Leu	Lys	Gln	Leu	Glu	Asp	Arg	Cys	Thr	Glu	Gln	Lys	Leu	Ser
145					150					155					160
Thr	Ala	Met	Arg	Ile	Thr	Lys	Trp	Lys	Glu	Lys	Val	Gln	Ile	Gln	Arg
				165					170					175	
Gln	Lys	Ile	Arg	Ser	Asp	Phe	Lys	Asn	Leu	Gln	Cys	Phe	Leu	His	Glu
			180					185					190		
Glu	Glu	Lys	Ser	Tyr	Leu	Trp	Arg	Leu	Glu	Lys	Glu	Glu	Gln	Gln	Thr
		195					200					205			
Leu	Ser	Arg	Leu	Arg	Asp	Tyr	Glu	Ala	Gly	Leu	Gly	Leu	Lys	Ser	Asn
	210					215					220				
Glu	Leu	Lys	Ser	His	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Cys	Gln	Gly	Ser
225					230					235					240
Ala	Gln	Lys	Leu	Leu	Gln	Asn	Val	Asn	Asp	Thr	Leu	Ser	Arg	Ser	Trp
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Ala	Val	Lys	Leu	Glu	Thr	Ser	Glu	Ala	Val	Ser	Leu	Glu	Leu	His	Thr

260

265

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
 275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
 290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
 305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
 325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
 340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
 355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
 370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
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Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
 450 455 460

Asp
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<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477).. (1871)

<400> 98

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ccttgggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca	ctggagga	ctagcctgcc	aggaatacac	gtcttcaga	aaagttctgt	240										
gtggcttcaa	gagactgac	aaattgtgag	aggaaaacag	cctaccocgt	cctcttttct	300										
tcaatacaaa	atgagataat	aggggttgg	aggaaaacct	tcaagaccta	tggaagtcag	360										
ttgcagccag	ctcatcacat	agaggtgcag	gtgaggtgta	ttttcatcac	ggtggaaaat	420										
tctggctgct	tcattctccat	ctctagagcc	aatattggag	cttttcaata	aaagct atg	479										
					Met											
					1											
gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc	527															
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser																
	5					10									15	
atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac	575															
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His																
	20					25							30			
agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa	623															
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln																
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aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca	671															
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro																
	50				55				60						65	
ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att	719															
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile																
			70						75					80		
gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga	767															
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly																
			85					90					95			
gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg	815															
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp																
		100					105					110				
cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt	863															
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val																
	115					120					125					
gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca	911															
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr																
	130				135					140					145	
aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca	959															
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr																
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gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa	1007															
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln																
			165					170					175			
aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa	1055															
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu																

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu 195 200 205	1103
agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu 210 215 220 225	1151
ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala 230 235 240	1199
cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala 245 250 255	1247
gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met 260 265 270	1295
tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser 275 280 285	1343
cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu 290 295 300 305	1391
att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu 310 315 320	1439
aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu 325 330 335	1487
ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val 340 345 350	1535
ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln 355 360 365	1583
agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu 370 375 380 385	1631
agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr 390 395 400	1679
tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp 405 410 415	1727

tat gag gcc gga gtt tcc ttt tat aac ggg aat act tgc cac 1775
 Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
 420 425 430
 atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823
 Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
 435 440 445
 ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
 Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
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<210> 99
 <211> 465
 <212> PRT
 <213> Homo sapiens

<400> 99
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 35 40 45
 Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
 50 55 60
 Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
 65 70 75 80
 Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
 85 90 95
 Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
 100 105 110
 Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
 115 120 125
 Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val
 130 135 140
 Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
 145 150 155 160
 Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
 165 170 175
 Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
 180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
 195 200 205
 Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
 210 215 220
 Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
 225 230 235 240
 Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
 245 250 255
 Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
 260 265 270
 Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
 275 280 285
 Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
 290 295 300
 Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
 305 310 315 320
 Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
 325 330 335
 Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
 340 345 350
 Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
 355 360 365
 Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
 370 375 380
 Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400
 Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415
 Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430
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 450 455 460
 Asp
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<210> 100
 <211> 1940

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (477).. (1871)

<400> 100

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ccttgggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180
tggtgtatca ctggaggaaa tagcctgcc aaggaatacac gtcttcagaa gaagttctgt 240
gtggcttcaa gagactgata aaattgtgag aggaaaacag cctaccgggt cctcttttct 300
tcaatacaaaa atgagataat aggggttggg aggaaaacct tcaagaccta tggaagtcag 360
ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcacac ggtggaaaat 420
tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg 479
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gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
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atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
20 25 30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
35 40 45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
50 55 60 65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
70 75 80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
85 90 95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
100 105 110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
115 120 125

gaa gac gta tgc caa ctc tac aag gaa aag ctc cag aaa gtg aca	911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr	
130 135 140 145	
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Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr	
150 155 160	
gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa	1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln	
165 170 175	
aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa	1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu	
180 185 190	
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Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu	
195 200 205	
agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa	1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu	
210 215 220 225	
ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc	1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala	
230 235 240	
cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct	1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala	
245 250 255	
gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg	1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met	
260 265 270	
tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt	1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser	
275 280 285	
cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta	1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu	
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Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu	
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Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu	
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Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val	
340 345 350	
ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag	1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln	

355

360

365

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 370 375 380

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 Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr 400
 390 395

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727
 Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp 415
 405 410

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775
 Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His 430
 420 425

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823
 Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr 445
 435 440

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
 Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp 465
 450 455 460

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag 1940

<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
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Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
 20 25 30

Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
 35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
 50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
 65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
 85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
 100 105 110

Ile Pro His Ser Arg Ala Lys Pro His Gln Arg Glu Leu Ile Asp
 115 120 125
 Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
 130 135 140
 Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
 145 150 155 160
 Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
 165 170 175
 Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
 180 185 190
 Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
 195 200 205
 Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
 210 215 220
 Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
 225 230 235 240
 Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
 245 250 255
 His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
 260 265 270
 Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
 275 280 285
 Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
 290 295 300
 Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
 305 310 315 320
 Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
 325 330 335
 Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
 340 345 350
 Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
 355 360 365
 Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
 370 375 380
 His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
 385 390 395 400
 Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
 405 410 415
 Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
 435 440 445
 Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
 450 455 460
 Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
 465 470 475 480
 Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
 485 490 495
 Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
 500 505 510
 Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
 515 520 525
 Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
 530 535 540
 His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
 545 550 555 560
 Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
 565 570 575
 His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
 580 585 590
 Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
 595 600 605
 Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
 610 615 620
 Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
 625 630 635 640
 Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
 645 650 655
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 660 665 670
 Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
 675 680 685

<210> 102
 <211> 2783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (128)... (2182)

<400> 102

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cggccggctc ggacgtgtga ccgcgctag ggggtggcag cgggcagtgc ggggcggcaa 120
ggcgcacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169
Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser
1 5 10
acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217
Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser
15 20 25 30
aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265
Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln
35 40 45
tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313
Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His
50 55 60
tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361
Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr
65 70 75
ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca 409
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala
80 85 90
aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca 457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala
95 100 105 110
aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag 505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys
115 120 125
att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta 553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val
130 135 140
gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601
Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu
145 150 155
ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649
Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg
160 165 170
aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697
Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val
175 180 185 190
tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745
Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu
195 200 205

aaa cta ggg aac ttt tt att aat gaa gcc atg gaa cta aat gtt ggg Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly	793
210 215 220	
gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg	841
225 230 235	
acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys	889
240 245 250	
caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met	937
255 260 265 270	
tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys	985
275 280 285	
gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser	1033
290 295 300	
ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn	1081
305 310 315	
cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe	1129
320 325 330	
ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr	1177
335 340 345 350	
gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys	1225
355 360 365	
gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile	1273
370 375 380	
gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu	1321
385 390 395	
agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His	1369
400 405 410	
agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser	1417
415 420 425 430	
gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg	1465

Gly Thr Pro Ala Val	Asn Lys Gln Gln Ile Gly Asp	Ile Arg	
435	440	445	
atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc			1513
Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys			
450	455	460	
ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt			1561
Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val			
465	470	475	
ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa			1609
Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys			
480	485	490	
gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac			1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr			
495	500	505	
tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt			1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly			
515	520	525	
gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa			1753
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys			
530	535	540	
aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca			1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala			
545	550	555	
aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac			1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr			
560	565	570	
ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct			1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro			
575	580	585	
agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta			1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu			
595	600	605	
aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag			1993
Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln			
610	615	620	
gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat			2041
Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn			
625	630	635	
gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act			2089
Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr			
640	645	650	
ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa			2137
Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys			
655	660	665	
670			

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgc aac 2182
 Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
 675 680 685
 tgaaagactt ttggaatgga ccctatggga ctctctttt ccactgtgag atctacaggg 2242
 aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302
 attcccctgt ggctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362
 actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422
 ggtttttcag acaattttgc agaaagggtgc attgattctt aaattctctc tgttgagagc 2482
 atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaaggagg 2542
 gaagctccca tgttgtttaa aggctgtaat tggagcagct tttggctgcg taactgtgaa 2602
 ctatggccat atataatttt ttttcattaa ttttgaaga tacttgtggc tggaaaagtg 2662
 cattccttgt taataaactt tttatttatt acagcccaaa gagcagtatt tattatcaaa 2722
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 g 2783

<210> 103
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 103
 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
 1 5 10 15
 Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
 20 25 30
 Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
 35 40 45
 Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
 50 55 60
 Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
 65 70 75 80
 Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
 85 90 95
 Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
 100 105 110
 Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
 115 120 125

Ala Gly Cys Cys Phe Pro Phe Cys Val Asp Ala Leu Asp Val
 130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
 145 150 155 160

Leu

<210> 104
 <211> 1589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (70).. (552)

<400> 104
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ggcggtaaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
 1 5 10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159
 Ser Ala Pro Ser Ala Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
 Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
 35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
 Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
 50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
 Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
 65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351
 Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met
 80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
 Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
 115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
 130 135 140

gac gtg gac cat ta t ccc aac tgc aga gct ctc ctg acc tac 543
 Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
 145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
 Lys Arg Leu
 160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga ggttctgccc tgggtggtctc 652
 acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712
 aaatctccaa accccagaaa ttgctgcttg gactcgtgca taggacttgc aaagacattc 772
 cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832
 ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892
 ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952
 ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012
 ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072
 tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaattttt 1132
 tttttaaata caaggagggg gctattaaca ccagtacag acatatccac aaggctcgtaa 1192
 atgcatgcta gaaaaatagg gctggatctt atcaactgcc tgtctcccct tgtttctctg 1252
 tgccagatct tcagtgtccc tttccataca gggatttttt tctcatagag taatttatatg 1312
 aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt ctttttttta 1372
 aaaaaaaca gagatggggg cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432
 aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
 tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552
 tggtgtcatt ttcccatttg ccaatgtagt ctcaatt 1589

<210> 105
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 105
 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
 1 5 10 15
 Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
 20 25 30
 Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
 35 40 45

Thr Gly Pro Asp Gls Gly Met Asn Pro Pro Ser Tyr Thr Gln
 50 55 60
 Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
 65 70 75 80
 Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
 85 90 95
 Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
 100 105 110
 Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
 115 120 125
 Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
 130 135 140
 Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
 145 150 155 160
 Leu

<210> 106
 <211> 1589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (70).. (552)

<400> 106
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 ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
 Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
 1 5 10
 tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159
 Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15 20 25 30
 agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
 Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
 35 40 45
 ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
 Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
 50 55 60
 acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
 Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
 65 70 75
 gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351

Val Tyr Val Gln His Ile Thr Phe Leu Asp Arg Pro Val In Met
80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
Lys Arg Leu
160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga ggttctgccc tgggtggtctc 652
acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712
aaatctccaa accccagaaa ttgctgcttg gagtctgca taggacttgc aaagacattc 772
cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832
ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892
ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952
ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012
ccgtctcttc ccgtccctga tgacaaagat ctgacctac agactttaca ggcttggtt 1072
tgagattctg taactgcaga ctccattagc acacagattc actttaattt ctttaattttt 1132
tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192
atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctccct tgtttctctg 1252
tgccagatct tcagtgtccc tttccataca gggatttttt tctcatagag taattatatg 1312
aacagttttt atgacctcct ttggtctga aatactttcg aacagaattt ctttttttta 1372
aaaaaaaaa gagatggggg ctactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432
aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552
tggtgtcatt ttccatttg ccaatgtagt ctcaatt 1589

<210> 107
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 107

Met	Ala	Ser	Ala	Ser	Gly	Ala	Met	Ala	Lys	His	Glu	Gln	Ile	Leu	Val
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Leu	Asp	Pro	Pro	Thr	Asp	Leu	Lys	Phe	Lys	Gly	Pro	Phe	Thr	Asp	Val
			20					25					30		
Val	Thr	Thr	Asn	Leu	Lys	Leu	Arg	Asn	Pro	Ser	Asp	Arg	Lys	Val	Cys
			35				40					45			
Phe	Lys	Val	Lys	Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn
	50					55					60				
Ser	Gly	Ile	Ile	Asp	Pro	Gly	Ser	Thr	Val	Thr	Val	Ser	Val	Met	Leu
65					70					75					80
Gln	Pro	Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met
				85					90					95	
Val	Gln	Thr	Ile	Phe	Ala	Pro	Pro	Asn	Thr	Ser	Asp	Met	Glu	Ala	Val
			100					105					110		
Trp	Lys	Glu	Ala	Lys	Pro	Asp	Glu	Leu	Met	Asp	Ser	Lys	Leu	Arg	Cys
		115					120					125			
Val	Phe	Glu	Met	Pro	Asn	Glu	Asn	Asp	Lys	Leu	Asn	Asp	Met	Glu	Pro
	130					135					140				
Ser	Lys	Ala	Val	Pro	Leu	Asn	Ala	Ser	Lys	Gln	Asp	Gly	Pro	Met	Pro
145					150					155					160
Lys	Pro	His	Ser	Val	Ser	Leu	Asn	Asp	Thr	Glu	Thr	Arg	Lys	Leu	Met
				165					170					175	
Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Met	Met	Lys	Leu	Ser	Glu	Glu
			180					185					190		
Asn	Arg	His	Leu	Arg	Asp	Glu	Gly	Leu	Arg	Leu	Arg	Lys	Val	Ala	His
		195					200					205			
Ser	Asp	Lys	Pro	Gly	Ser	Thr	Ser	Thr	Ala	Ser	Phe	Arg	Asp	Asn	Val
	210					215					220				
Thr	Ser	Pro	Leu	Pro	Ser	Leu	Leu	Val	Val	Ile	Ala	Ala	Ile	Phe	Ile
225					230					235					240
Gly	Phe	Phe	Leu	Gly	Lys	Phe	Ile	Leu							
				245											

<210> 108
 <211> 1595
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232).. (978)

<400> 108

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gacccagcgg gtggcccacc gaaccggtga cacagcggca ggcgtaggg ctcgggagcc 120
gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgcccc 180
agtcagcaaa ccgccgccgc gggcgcgccc ccgctctcgc ctgtctctcc g atg gcg 237
Met Ala
1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285
Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp
5 10 15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333
Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr
20 25 30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381
Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys
35 40 45 50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429
Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly
55 60 65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477
Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro
70 75 80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln
85 90 95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573
Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys
100 105 110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621
Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe
115 120 125 130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669
Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys
135 140 145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717
Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro
150 155 160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765

His Ser Val Ser Leu n Asp Thr Glu Thr Arg Lys Leu n Glu Glu
 165 170 175
 tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813
 Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg
 180 185 190
 cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861
 His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp
 195 200 205 210
 aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909
 Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser
 215 220 225
 cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957
 Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe
 230 235 240
 ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttcct 1008
 Phe Leu Gly Lys Phe Ile Leu
 245
 tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcac tggtagtatg 1068
 gcccacgggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128
 cttacgggta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188
 ccagatcatc actagcagat gtcagttgca cattgagtc tttatgaaat tcataaataa 1248
 agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308
 tgttattttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368
 atttagattg ctaatcccac tcattcagga aatgccaaga ggtatttcctt ggggaaatgg 1428
 tgccctttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488
 cttatccctt gtgaggcagt tgttgactga gtttttcac cttacaatcc tgtcccatgg 1548
 tatttaacat aaaaaaaaaat aaaactgtta acagattcct gctcgat 1595

<210> 109
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 109
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 20 25 30
 Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
 35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
 50 55 60
 His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65 70 75 80
 Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
 85 90 95
 Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
 100 105 110
 Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
 115 120 125
 Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
 130 135 140
 Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
 145 150 155 160
 Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
 165 170 175
 Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
 180 185 190
 Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
 195 200 205
 Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
 210 215 220
 Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
 225 230 235 240
 Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
 245 250 255
 Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
 260 265 270
 Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
 275 280 285
 Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
 290 295 300
 Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
 305 310 315 320
 Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
 325 330 335
 Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
 340 345 350

Asn Asn His Thr Cys Trp Lys Ala Trp Glu Asp Thr Asp Lys
 355 360 365
 Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
 370 375 380
 Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
 385 390 395 400
 Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg
 405 410 415
 Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
 420 425 430
 Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
 435 440 445
 Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
 450 455 460
 Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
 465 470 475 480
 Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
 485 490 495
 Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
 500 505 510
 Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
 515 520 525
 Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
 530 535 540

<210> 110
 <211> 1810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (102).. (1721)

<400> 110
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 gaggacccac ctctgagtgt ccagtgggtca gttgcccag g atg ggg acc aca gcc 116
 Met Gly Thr Thr Ala
 1 5
 aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164
 Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
 10 15 20
 gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr	25	Ala Thr Gly Gln Arg Gln Leu Arg	30	Glu His	35	
ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga						260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg	40	45	50			
agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt						308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe	55	60	65			
gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct						356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro	70	75	80	85		
ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa						404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu	90	95	100			
gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg						452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu	105	110	115			
ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca						500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro	120	125	130			
ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag						548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln	135	140	145			
cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat						596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp	150	155	160	165		
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc						644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys	170	175	180			
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag						692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln	185	190	195			
tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg						740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu	200	205	210			
gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc						788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg	215	220	225			
cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt						836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys	230	235	240	245		
gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg						884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg	250	255	260			

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro	932
265 270 275	
cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tgc His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser	980
280 285 290	
ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile	1028
295 300 305	
aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu	1076
310 315 320 325	
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu	1124
330 335 340	
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys	1172
345 350 355	
aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu	1220
360 365 370	
tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser	1268
375 380 385	
cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr	1316
390 395 400 405	
gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu	1364
410 415 420	
atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His	1412
425 430 435	
att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro	1460
440 445 450	
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile	1508
455 460 465	
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu	1556
470 475 480 485	
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc	1604

Cys Cys Tyr Leu Ser Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
 490 495 500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652
 Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
 505 510 515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700
 Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
 520 525 530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751
 Thr Ser Glu Pro Lys Glu Glu
 535 540

tggggggaac cccaccctgc cccaccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 111
 Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
 1 5 10 15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
 20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
 35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
 50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
 85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
 100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
 115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
 130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
 145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
 165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
 195 200 205
 Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
 210 215 220
 Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
 225 230 235 240
 Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
 245 250 255
 Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
 260 265 270
 Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
 275 280 285
 Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
 290 295 300
 Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
 305 310 315 320
 Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
 325 330 335
 Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
 340 345 350
 Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
 355 360 365
 Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
 370 375 380
 Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
 385 390 395 400
 Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
 405 410 415
 Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
 420 425 430
 Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
 435 440 445
 Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
 450 455 460
 Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
 465 470 475 480
 Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
 485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
 500 505 510
 Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
 515 520 525
 Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
 530 535 540

<210> 112
 <211> 1810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (102).. (1721)

<400> 112
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 gaggacccac ctctgagtgt ccagtgggtca gttgcccag g atg ggg acc aca gcc 116
 Met Gly Thr Thr Ala
 1 5
 aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164
 Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
 10 15 20
 gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212
 Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
 25 30 35
 ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
 Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
 40 45 50
 agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
 Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
 55 60 65
 gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
 Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
 70 75 80 85
 ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
 Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
 90 95 100
 gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452
 Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
 105 110 115
 ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500
 Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
 120 125 130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln 135 140 145	548
cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp 150 155 160 165	596
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys 170 175 180	644
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln 185 190 195	692
tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu 200 205 210	740
gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg 215 220 225	788
cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys 230 235 240 245	836
gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg 250 255 260	884
cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro 265 270 275	932
cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser 280 285 290	980
ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile 295 300 305	1028
aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu 310 315 320 325	1076
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu 330 335 340	1124
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys 345 350 355	1172
aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag	1220

Thr	Trp	Lys	Ala	Trp	Leu	Asp	Thr	Leu	Asp	Lys	Tyr	Cys	Arg	Glu		
		360					365					370				
tat	gct	gtg	aag	acc	cac	cac	cac	tgt	tgt	tgc	cgc	cac	cct	ccc	agc	1268
Tyr	Ala	Val	Lys	Thr	His	His	His	Leu	Cys	Cys	Arg	His	Pro	Pro	Ser	
	375					380					385					
cct	act	cgg	gat	gag	tgc	ttt	gcc	cgt	cgg	gct	cct	tac	ccc	aac	tat	1316
Pro	Thr	Arg	Asp	Glu	Cys	Phe	Ala	Arg	Arg	Ala	Pro	Tyr	Pro	Asn	Tyr	
	390				395					400					405	
gac	cgg	gac	atc	ttg	acc	att	gac	atc	agt	cga	gtc	acc	ccc	aac	ctc	1364
Asp	Arg	Asp	Ile	Leu	Thr	Ile	Asp	Ile	Ser	Arg	Val	Thr	Pro	Asn	Leu	
			410						415					420		
atg	ggc	cac	ctc	tgt	gga	aac	caa	aga	gtt	ctc	acc	aag	cat	aaa	cat	1412
Met	Gly	His	Leu	Cys	Gly	Asn	Gln	Arg	Val	Leu	Thr	Lys	His	Lys	His	
			425					430					435			
att	cct	ggg	ctg	atc	cac	aac	atg	act	gcc	cgc	tgc	tgt	gac	ctg	cca	1460
Ile	Pro	Gly	Leu	Ile	His	Asn	Met	Thr	Ala	Arg	Cys	Cys	Asp	Leu	Pro	
		440					445					450				
ttt	cca	gaa	cag	gcc	tgc	tgt	gca	gag	gag	gag	aaa	tta	acc	ttc	atc	1508
Phe	Pro	Glu	Gln	Ala	Cys	Cys	Ala	Glu	Glu	Glu	Lys	Leu	Thr	Phe	Ile	
	455					460					465					
aat	gat	ctg	tgt	ggc	ccc	cga	cgt	aac	atc	tgg	cga	gac	cct	gcc	ctc	1556
Asn	Asp	Leu	Cys	Gly	Pro	Arg	Arg	Asn	Ile	Trp	Arg	Asp	Pro	Ala	Leu	
	470				475					480					485	
tgc	tgt	tac	ctg	agt	cct	ggg	gat	gaa	cag	gtc	aac	tgc	ttc	aac	atc	1604
Cys	Cys	Tyr	Leu	Ser	Pro	Gly	Asp	Glu	Gln	Val	Asn	Cys	Phe	Asn	Ile	
				490					495					500		
aat	tat	ctg	agg	aac	gtg	gct	cta	gtg	tct	gga	gac	act	gag	aac	gcc	1652
Asn	Tyr	Leu	Arg	Asn	Val	Ala	Leu	Val	Ser	Gly	Asp	Thr	Glu	Asn	Ala	
			505					510					515			
aag	ggc	cag	ggg	gag	cag	ggc	tca	act	gga	gga	aca	aat	atc	agc	tcc	1700
Lys	Gly	Gln	Gly	Glu	Gln	Gly	Ser	Thr	Gly	Gly	Thr	Asn	Ile	Ser	Ser	
		520					525					530				
acc	tct	gag	ccc	aag	gaa	gaa	tgagtc	cccc	cagagcc	cta	gagggtc	caga				1751
Thr	Ser	Glu	Pro	Lys	Glu	Glu										
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tg	ggg	gga	ac	ccc	ccctgc	ccc	acccatc	tga	acactca	ttacactaaa	cac	ctcttg				1810

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 <211> 382
 <212> PRT
 <213> Homo sapiens

<400> 113
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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
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 Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
 35 40 45
 Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
 50 55 60
 Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
 65 70 75 80
 Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
 85 90 95
 Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
 100 105 110
 Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
 115 120 125
 Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
 130 135 140
 Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
 145 150 155 160
 Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
 165 170 175
 Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
 180 185 190
 Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
 195 200 205
 Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
 210 215 220
 Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
 225 230 235 240
 Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
 245 250 255
 Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
 260 265 270
 Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
 275 280 285
 Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
 290 295 300
 Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
 305 310 315 320

Lys	Lys	Glu	Glu	Glu	Lys	Val	Ala	Gln	Thr	Asp	Gly	Val	Asn	Val		
		110				115					120					
gac	atg	cac	ttg	aag	cag	att	gag	ata	aag	aag	ttc	aag	tac	ggg	att	617
Asp	Met	His	Leu	Lys	Gln	Ile	Glu	Ile	Lys	Lys	Phe	Lys	Tyr	Gly	Ile	
	125					130					135					
gaa	gag	cat	ggg	aag	gtg	aaa	atg	cga	ggg	ggg	ttg	ctg	cga	acc	tac	665
Glu	Glu	His	Gly	Lys	Val	Lys	Met	Arg	Gly	Gly	Leu	Leu	Arg	Thr	Tyr	
140					145					150					155	
atc	atc	agt	atc	ctc	ttc	aag	tct	atc	ttt	gag	gtg	gcc	ttc	ttg	ctg	713
Ile	Ile	Ser	Ile	Leu	Phe	Lys	Ser	Ile	Phe	Glu	Val	Ala	Phe	Leu	Leu	
				160					165					170		
atc	cag	tgg	tac	atc	tat	gga	ttc	agc	ttg	agt	gct	gtt	tac	act	tgc	761
Ile	Gln	Trp	Tyr	Ile	Tyr	Gly	Phe	Ser	Leu	Ser	Ala	Val	Tyr	Thr	Cys	
			175					180					185			
aaa	aga	gat	ccc	tgc	cca	cat	cag	gtg	gac	tgt	ttc	ctc	tct	cgc	ccc	809
Lys	Arg	Asp	Pro	Cys	Pro	His	Gln	Val	Asp	Cys	Phe	Leu	Ser	Arg	Pro	
		190					195					200				
acg	gag	aaa	acc	atc	ttc	atc	atc	ttc	atg	ctg	gtg	gtg	tcc	ttg	gtg	857
Thr	Glu	Lys	Thr	Ile	Phe	Ile	Ile	Phe	Met	Leu	Val	Val	Ser	Leu	Val	
	205					210					215					
tcc	ctg	gcc	ttg	aat	atc	att	gaa	ctc	ttc	tat	gtt	ttc	ttc	aag	ggc	905
Ser	Leu	Ala	Leu	Asn	Ile	Ile	Glu	Leu	Phe	Tyr	Val	Phe	Phe	Lys	Gly	
220					225					230					235	
gtt	aag	gat	cgg	gtt	aag	gga	aag	agc	gac	cct	tac	cat	gcg	acc	agt	953
Val	Lys	Asp	Arg	Val	Lys	Gly	Lys	Ser	Asp	Pro	Tyr	His	Ala	Thr	Ser	
				240					245					250		
ggg	gag	ctg	agc	cct	gcc	aaa	gac	tgt	ggg	tct	caa	aaa	tat	gct	tat	1001
Gly	Ala	Leu	Ser	Pro	Ala	Lys	Asp	Cys	Gly	Ser	Gln	Lys	Tyr	Ala	Tyr	
			255					260					265			
ttc	aat	ggc	tgc	tcc	tca	cca	acc	gct	ccc	ctc	tcg	cct	atg	tct	cct	1049
Phe	Asn	Gly	Cys	Ser	Ser	Pro	Thr	Ala	Pro	Leu	Ser	Pro	Met	Ser	Pro	
		270					275					280				
cct	ggg	tac	aag	ctg	gtt	act	ggc	gac	aga	aac	aat	tct	tct	tgc	cgc	1097
Pro	Gly	Tyr	Lys	Leu	Val	Thr	Gly	Asp	Arg	Asn	Asn	Ser	Ser	Cys	Arg	
	285					290					295					
aat	tac	aac	aag	caa	gca	agt	gag	caa	acc	tgg	gct	aat	tac	agt	gca	1145
Asn	Tyr	Asn	Lys	Gln	Ala	Ser	Glu	Gln	Thr	Trp	Ala	Asn	Tyr	Ser	Ala	
300					305					310					315	
gaa	caa	aat	cga	atg	ggg	cag	gcg	gga	agc	acc	atc	tct	aac	tcc	cat	1193
Glu	Gln	Asn	Arg	Met	Gly	Gln	Ala	Gly	Ser	Thr	Ile	Ser	Asn	Ser	His	
				320					325					330		
gca	cag	cct	ttt	gat	ttc	ccc	gat	gat	aac	cag	aat	tct	aaa	aaa	cta	1241
Ala	Gln	Pro	Phe	Asp	Phe	Pro	Asp	Asp	Asn	Gln	Asn	Ser	Lys	Lys	Leu	
			335				340						345			

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
365 370 375

ctg gag atc tagatacagg ctigaaagca tcaagattcc actcaattgt 1386
Leu Glu Ile
380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cgggtggaggt 1446
ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506
tactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566
gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626
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ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106
ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata ttaacaatc 2166
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agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826
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ttagtat 3074

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<212> PRT
<213> Homo sapiens

<400> 115

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
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Arg Ile Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
35 40 45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
50 55 60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
 210 215 220
 Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
 225 230 235 240
 Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
 245 250 255
 Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
 260 265 270
 Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
 275 280 285
 Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
 290 295 300
 Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
 305 310 315 320
 Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
 325 330 335
 Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
 340 345 350
 Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
 355 360 365
 Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
 370 375 380

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<220>
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 attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180
 aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
 Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
 1 5 10
 gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281
 Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
 15 20 25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca	329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser	
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gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct	377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro	
45 50 55	
ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg	425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val	
60 65 70 75	
cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg	473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu	
80 85 90	
tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac	521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn	
95 100 105	
aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg	569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val	
110 115 120	
gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att	617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile	
125 130 135	
gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac	665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr	
140 145 150 155	
atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg	713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu	
160 165 170	
atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc	761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys	
175 180 185	
aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc	809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro	
190 195 200	
acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg	857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val	
205 210 215	
tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc	905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly	
220 225 230 235	
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt	953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser	
240 245 250	
ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat	1001

Gly Ala Leu Ser Pro [REDACTED] Lys Asp Cys Gly Ser Gln Lys [REDACTED] Ala Tyr
 255 260 265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049
 Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
 270 275 280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
 Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
 285 290 295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145
 Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala
 300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
 Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
 320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
 Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
 335 340 345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
 Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
 350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
 Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
 365 370 375

ctg gag atc tagatacagg ctgaaagca tcaagattcc actcaattgt 1386
 Leu Glu Ile
 380

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 agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826
 cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886
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 <213> Homo sapiens

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 35 40 45
 Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
 50 55 60
 Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
 65 70 75 80
 Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
 100 105 110
 Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
 115 120 125
 Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
 130 135 140
 Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
 145 150 155 160
 Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
 165 170 175
 Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
 180 185 190
 Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
 195 200 205
 Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
 210 215 220
 Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
 225 230 235 240
 His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
 245 250 255
 Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
 260 265 270
 Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
 275 280 285
 Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
 290 295 300
 Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
 305 310 315 320
 Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
 325 330 335
 Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
 340 345 350
 Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
 355 360 365
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 370 375 380
 Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
 385 390 395

<210> 118
 <211> 2054
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (76).. (1269)

<400> 118

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          Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
              1              5              10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159
Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu
          15              20              25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207
Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
          30              35              40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255
Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
          45              50              55              60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303
Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
          65              70              75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351
Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
          80              85              90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
          95              100              105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
          110              115              120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
          125              130              135              140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
          145              150              155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
          160              165              170

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190 195 200	
ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu	735
205 210 215 220	
acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr	783
225 230 235	
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys	831
240 245 250	
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu	879
255 260 265	
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg	927
270 275 280	
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser	975
285 290 295 300	
gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu	1023
305 310 315	
cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly	1071
320 325 330	
gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp	1119
335 340 345	
gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys	1167
350 355 360	
tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu	1215
365 370 375 380	
aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln	1263
385 390 395	
gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca Glu Leu	1319

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379
 gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439
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 cccttgtcct cctgggggca tatctcagtc aggacgcggc ttctgatga tggtcgttgg 1739
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 aactgaagg gcagggtggg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859
 gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919
 cttacccggg aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979
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 actcacctac tcatac 2054

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 <212> PRT
 <213> Homo sapiens

<400> 119
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 Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala
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 Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
 35 40 45
 Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
 50 55 60
 Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
 65 70 75 80
 Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
 85 90 95
 Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
 100 105 110
 Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
 115 120 125

Trp His Asp Lys Gly ████ n Gln Tyr Arg Asn Trp Phe Leu ████ Glu Phe
 130 135 140
 Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
 145 150 155 160
 Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
 165 170 175
 Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
 180 185 190
 Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
 195 200 205
 Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
 210 215 220
 Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
 225 230 235 240
 His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
 245 250 255
 Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
 260 265 270
 Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
 275 280 285
 Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
 290 295 300
 Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
 305 310 315 320
 Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
 325 330 335
 Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
 340 345 350
 Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
 355 360 365
 Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
 370 375 380
 Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
 385 390 395

<210> 120
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<220>

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 <222> (76).. (1269)

<400> 120

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 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
 1 5 10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159
 Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu
 15 20 25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207
 Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
 30 35 40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255
 Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45 50 55 60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303
 Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
 65 70 75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351
 Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
 80 85 90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
 Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
 95 100 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
 Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
 110 115 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
 Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
 125 130 135 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
 Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
 145 150 155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
 Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
 160 165 170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
 Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
 175 180 185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
 Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
 190 195 200

ctt gta ctc ttg gaa t ggg atg gag ttg gga atc aca g gct ttg 735
 Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu 220
 205 210 215

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
 Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr 235
 225 230

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
 Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys 250
 240 245

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879
 Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu 265
 255 260

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927
 Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg 280
 270 275

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975
 Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser 300
 285 290 295

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023
 Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu 315
 305 310

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071
 Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly 330
 320 325

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119
 Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp 345
 335 340

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167
 Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys 360
 350 355

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215
 Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu 380
 365 370 375

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
 Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln 395
 385 390

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca 1319
 Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcaactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca ggggtccac tacagacca gcccagggtt caatgtcctc 1619
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 cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979
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 actcacctac tcatc 2054

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 <211> 108
 <212> PRT
 <213> Homo sapiens

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 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
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 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35 40 45
 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50 55 60
 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65 70 75 80
 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85 90 95
 Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
 100 105

<210> 122
 <211> 1546
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (89)..(412)
 <400> 122

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	Met Gly Val Gln Val Glu Thr Ile		
	1 5		
tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg			160
Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val			
10 15 20			
gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc			208
Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser			
25 30 35 40			
cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg			256
Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val			
45 50 55			
atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga			304
Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg			
60 65 70			
gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac			352
Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His			
75 80 85			
cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt			400
Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu			
90 95 100			
cta aaa ctg gaa tgacaggaat ggccctcctcc cttagctccc tgttcttgg			452
Leu Lys Leu Glu			
105			
tctgccatgg agggatctgg tgccctccaga catgtgcaca tgaatccata tggagctttt			512
cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc			572
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cacaagtggg aggttaacat tagaatagga attgggtgttg ggggggggggt ttgcaagaat			812
attttatttt aatttttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc			872
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gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca			1172

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<210> 123
 <211> 679
 <212> PRT
 <213> Homo sapiens

<400> 123

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Pro	Leu	Val	Asp	Tyr	Leu	Trp	Met	Leu	Ile	Leu	Gly	Phe	Ile	Ile	Ala
			20					25					30		
Phe	Val	Leu	Ala	Phe	Ser	Val	Gly	Ala	Asn	Asp	Val	Ala	Asn	Ser	Phe
		35					40					45			
Gly	Thr	Ala	Val	Gly	Ser	Gly	Val	Val	Thr	Leu	Lys	Gln	Ala	Cys	Ile
	50					55					60				
Leu	Ala	Ser	Ile	Phe	Glu	Thr	Val	Gly	Ser	Val	Leu	Leu	Gly	Ala	Lys
	65				70					75					80
Val	Ser	Glu	Thr	Ile	Arg	Lys	Gly	Leu	Ile	Asp	Val	Glu	Met	Tyr	Asn
				85					90					95	
Ser	Thr	Gln	Gly	Leu	Leu	Met	Ala	Gly	Ser	Val	Ser	Ala	Met	Phe	Gly
			100					105					110		
Ser	Ala	Val	Trp	Gln	Leu	Val	Ala	Ser	Phe	Leu	Lys	Leu	Pro	Ile	Ser
		115					120					125			
Gly	Thr	His	Cys	Ile	Val	Gly	Ala	Thr	Ile	Gly	Phe	Ser	Leu	Val	Ala
	130					135					140				
Lys	Gly	Gln	Glu	Gly	Val	Lys	Trp	Ser	Glu	Leu	Ile	Lys	Ile	Val	Met
	145				150					155					160
Ser	Trp	Phe	Val	Ser	Pro	Leu	Leu	Ser	Gly	Ile	Met	Ser	Gly	Ile	Leu
				165					170					175	
Phe	Phe	Leu	Val	Arg	Ala	Phe	Ile	Leu	His	Lys	Ala	Asp	Pro	Val	Pro
			180					185					190		
Asn	Gly	Leu	Arg	Ala	Leu	Pro	Val	Phe	Tyr	Ala	Cys	Thr	Val	Gly	Ile

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
 210 215 220
 Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
 225 230 235 240
 Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
 245 250 255
 Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
 260 265 270
 Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
 275 280 285
 Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
 290 295 300
 Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
 305 310 315 320
 Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
 325 330 335
 Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
 340 345 350
 Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
 355 360 365
 Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
 370 375 380
 Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
 385 390 395 400
 Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
 405 410 415
 Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
 420 425 430
 Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
 435 440 445
 Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
 450 455 460
 Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
 465 470 475 480
 Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
 485 490 495
 Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
 500 505 510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
 515 520 525
 Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
 530 535 540
 Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr
 545 550 555 560
 Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu
 565 570 575
 Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
 580 585 590
 Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
 595 600 605
 Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
 610 615 620
 Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
 625 630 635 640
 Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
 645 650 655
 Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
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 Arg Tyr Val Ile Leu Arg Met
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 <210> 124
 <211> 2916
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (81).. (2117)

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 Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala
 1 5 10
 acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161
 Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu
 15 20 25
 ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209
 Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp
 30 35 40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg	257
Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu	
45 50 55	
aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc	305
Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val	
60 65 70 75	
tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac	353
Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp	
80 85 90	
gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc	401
Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val	
95 100 105	
agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg	449
Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu	
110 115 120	
aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt	497
Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly	
125 130 135	
ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg	545
Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu	
140 145 150 155	
ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att	593
Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile	
160 165 170	
atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag	641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys	
175 180 185	
gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc	689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala	
190 195 200	
tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg	737
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro	
205 210 215	
ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg	785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser	
220 225 230 235	
gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt	833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys	
240 245 250	
ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct	881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser	
255 260 265	
gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa	929



Glu	Ser	Pro	Leu	Met		Lys	Lys	Asn	Ser	Leu	Lys	Glu	Asn	His	Glu		
		270					275					280					
gaa	aca	aag	ttg	tct	gtt	ggt	gat	att	gaa	aac	aag	cat	cct	gtt	tct		977
Glu	Thr	Lys	Leu	Ser	Val	Gly	Asp	Ile	Glu	Asn	Lys	His	Pro	Val	Ser		
	285					290					295						
gag	gta	ggg	cct	gcc	act	gtg	ccc	ctc	cag	gct	gtg	gtg	gag	gag	aga		1025
Glu	Val	Gly	Pro	Ala	Thr	Val	Pro	Leu	Gln	Ala	Val	Val	Glu	Glu	Arg		
	300				305					310					315		
aca	gtc	tca	ttc	aaa	ctt	gga	gat	ttg	gag	gaa	gct	cca	gag	aga	gag		1073
Thr	Val	Ser	Phe	Lys	Leu	Gly	Asp	Leu	Glu	Glu	Ala	Pro	Glu	Arg	Glu		
				320					325					330			
agg	ctt	ccc	agc	gtg	gac	ttg	aaa	gag	gaa	acc	agc	ata	gat	agc	acc		1121
Arg	Leu	Pro	Ser	Val	Asp	Leu	Lys	Glu	Glu	Thr	Ser	Ile	Asp	Ser	Thr		
			335					340					345				
gtg	aat	ggt	gca	gtg	cag	ttg	cct	aat	ggg	aac	ctt	gtc	cag	ttc	agt		1169
Val	Asn	Gly	Ala	Val	Gln	Leu	Pro	Asn	Gly	Asn	Leu	Val	Gln	Phe	Ser		
	350					355						360					
caa	gcc	gtc	agc	aac	caa	ata	aac	tcc	agt	ggc	cac	tac	cag	tat	cac		1217
Gln	Ala	Val	Ser	Asn	Gln	Ile	Asn	Ser	Ser	Gly	His	Tyr	Gln	Tyr	His		
	365					370				375							
acc	gtg	cat	aag	gat	tcc	ggc	ctg	tac	aaa	gag	cta	ctc	cat	aaa	tta		1265
Thr	Val	His	Lys	Asp	Ser	Gly	Leu	Tyr	Lys	Glu	Leu	Leu	His	Lys	Leu		
	380				385					390					395		
cat	ctt	gcc	aag	gtg	gga	gat	tgc	atg	gga	gac	tcc	ggt	gac	aaa	ccc		1313
His	Leu	Ala	Lys	Val	Gly	Asp	Cys	Met	Gly	Asp	Ser	Gly	Asp	Lys	Pro		
				400					405					410			
tta	agg	cgc	aat	aat	agc	tat	act	tcc	tat	acc	atg	gca	ata	tgt	ggc		1361
Leu	Arg	Arg	Asn	Asn	Ser	Tyr	Thr	Ser	Tyr	Thr	Met	Ala	Ile	Cys	Gly		
			415					420					425				
atg	cct	ctg	gat	tca	ttc	cgt	gcc	aaa	gaa	ggt	gaa	cag	aag	ggc	gaa		1409
Met	Pro	Leu	Asp	Ser	Phe	Arg	Ala	Lys	Glu	Gly	Glu	Gln	Lys	Gly	Glu		
	430						435					440					
gaa	atg	gag	aag	ctg	aca	tgg	cct	aat	gca	gac	tcc	aag	aag	cga	att		1457
Glu	Met	Glu	Lys	Leu	Thr	Trp	Pro	Asn	Ala	Asp	Ser	Lys	Lys	Arg	Ile		
	445					450					455						
cga	atg	gac	agt	tac	acc	agt	tac	tgc	aat	gct	gtg	tct	gac	ctt	cac		1505
Arg	Met	Asp	Ser	Tyr	Thr	Ser	Tyr	Cys	Asn	Ala	Val	Ser	Asp	Leu	His		
	460				465					470					475		
tca	gca	tct	gag	ata	gac	atg	agt	gtc	aag	gca	gag	atg	ggt	cta	ggt		1553
Ser	Ala	Ser	Glu	Ile	Asp	Met	Ser	Val	Lys	Ala	Glu	Met	Gly	Leu	Gly		
				480					485					490			
gac	aga	aaa	gga	agt	aat	ggc	tct	cta	gaa	gaa	tgg	tat	gac	cag	gat		1601
Asp	Arg	Lys	Gly	Ser	Asn	Gly	Ser	Leu	Glu	Glu	Trp	Tyr	Asp	Gln	Asp		
			495					500					505				

aag cct gaa gtc tct ctc ttc cag ttc ctg cag atc ctt aca gcc	1649
Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala	
510 515 520	
tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att	1697
Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile	
525 530 535	
ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct	1745
Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser	
540 545 550 555	
tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt	1793
Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly	
560 565 570	
atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg	1841
Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met	
575 580 585	
ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa	1889
Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu	
590 595 600	
ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc	1937
Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro	
605 610 615	
atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg	1985
Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp	
620 625 630 635	
ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt	2033
Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe	
640 645 650	
atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc	2081
Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala	
655 660 665	
atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt	2127
Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met	
670 675	
tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga	2187
atgattacag tgtaaacaga agactgacaa gagtcttttt atttgggagc cagaggagg	2247
aagtgttact tgtgtataa ctgcttttgt gctaaatatg aattgtctca aaattagctg	2307
tgtaaaatag cccgggttcc actggctcct gctgaggtcc cctttccttc tgggctgtga	2367
attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt	2427
tgtctctgaa gatgacttgt gatttttttt tctttttttt aaacatgaa gagccgtttg	2487
acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt	2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607
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gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727
tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787
ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847
ttaaatggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907
agtttttag 2916

<210> 125
<211> 288
<212> PRT
<213> Homo sapiens

<400> 125
Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala
1 5 10 15
Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu
20 25 30
Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys
35 40 45
Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
50 55 60
Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
65 70 75 80
Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
85 90 95
Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
100 105 110
Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
115 120 125
Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
130 135 140
Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145 150 155 160
Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
165 170 175
Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
180 185 190

Pro Ala Val Arg Gl  g Val Ile Glu Glu Ala Lys Thr  Phe Leu
195 200 205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
210 215 220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225 230 235 240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
245 250 255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
260 265 270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
275 280 285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (944)

<400> 126

tcaacgctg cctcccctcg agcgtcctca ggcagccgc cgcccgcgga gccagcacga 60

acgagcccag caccggccgg .atg gag cgt ccg caa ccc gac agc atg ccc cag 113
Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln
1 5 10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161
Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln
15 20 25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209
Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr
30 35 40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257
Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val
45 50 55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305
Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala
60 65 70 75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353
Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln
80 85 90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401
Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr
95 100 105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtc ggg cgc 449
 Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg
 110 115 120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497
 Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly
 125 130 135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545
 Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu
 140 145 150 155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593
 Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn
 160 165 170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641
 Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn
 175 180 185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689
 Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala
 190 195 200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737
 Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu
 205 210 215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785
 Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly
 220 225 230 235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833
 Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu
 240 245 250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881
 Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu
 255 260 265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929
 Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val
 270 275 280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984
 Gly Leu Tyr Ala Met
 285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggcttctt taccgtgggc 1044
 actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104
 ggagcctatg gcattcttccc caacgaaaag cacatccagg caatggccta aacttcagag 1164
 ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224
 acaccctaatt gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344
atgttgtgtc ttgtgttttt gtcttatttt tgttggagcc actctgttcc tggctcagcc 1404
tcaaatgcag ttttttgtt gtgttctgtt gtttttatag cagggttggg gtggtttttg 1464
agccatgcgt ggggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524
tgtgaaataa taaacaacat tgtctg 1550

<210> 127
<211> 135
<212> PRT
<213> Homo sapiens

<400> 127
Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu
1 5 10 15
Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val
20 25 30
Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro
35 40 45
Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
50 55 60
Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe
65 70 75 80
Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn
85 90 95
Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg
100 105 110
Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys
115 120 125
Ile Lys Cys Val Ala Phe Asp
130 135

<210> 128
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50).. (454)

<400> 128
cttctgacag ctggtgcgcc tgcccgggaa catcctcctg gactcaatc atg gct tgt 58
Met Ala Cys

ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106
 Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
 5 10 15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154
 Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
 20 25 30 35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202
 Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
 40 45 50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250
 Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
 55 60 65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
 Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
 70 75 80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
 Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
 85 90 95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
 Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
 100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442
 Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
 120 125 130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494
 Val Ala Phe Asp
 135

ctctgctccc ctg 507

<210> 129
 <211> 662
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn
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 Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn
 20 25 30
 Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp
 35 40 45
 Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys
 50 55 60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser
 65 70 75 80
 Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr
 85 90 95
 Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu
 100 105 110
 Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys
 115 120 125
 His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
 130 135 140
 Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
 145 150 155 160
 Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
 165 170 175
 Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
 180 185 190
 Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
 195 200 205
 Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
 210 215 220
 Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
 225 230 235 240
 Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
 245 250 255
 Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
 260 265 270
 Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
 275 280 285
 Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
 290 295 300
 Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
 305 310 315 320
 Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
 325 330 335
 Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
 340 345 350
 Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
 355 360 365

Glu Val Ala Glu Asn Met Gly Lys Cys His Leu Thr Lys Lys Gln
 370 375 380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp
 385 390 395 400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
 405 410 415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
 420 425 430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
 435 440 445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
 450 455 460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
 465 470 475 480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
 485 490 495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
 500 505 510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
 515 520 525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn
 530 535 540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
 545 550 555 560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln
 565 570 575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln
 580 585 590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn
 595 600 605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe
 610 615 620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn
 625 630 635 640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg
 645 650 655

Leu Arg Ile Ser Glu Lys
 660

<210> 130
 <211> 2251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (74).. (2059)

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 tcagtgggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag 109
 Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu
 1 5 10
 ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157
 Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys
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Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys
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Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp
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Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys
 65           70           75           80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu
          85           90           95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile
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Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu
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Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu
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Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr
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Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe
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Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr
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Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly
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Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg
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Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu
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Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr
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 Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
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 865 870 875 880
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 Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro
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 Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu
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 Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu
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 Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln
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 Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser
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Asp	Thr	Val	Cys	Leu	Ser	Val	Gly	Asp	Arg	Val	Pro	Ala	Asp	Leu	Arg	
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Ser	Glu	Phe	Gly	Glu	Val	Phe	Lys	Met	Met	Gln	Ala	Glu	Glu	Ala	Pro	
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Lys	Thr	Pro	Leu	Gln	Lys	Ser	Met	Asp	Leu	Leu	Gly	Lys	Gln	Leu	Ser	
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Phe	Tyr	Ser	Phe	Gly	Ile	Ile	Gly	Ile	Ile	Met	Leu	Val	Gly	Trp	Leu	
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Ala	Leu	Gly	Val	Met	Arg	Met	Val	Lys	Lys	Arg	Ala	Ile	Val	Lys	Lys	
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Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp	
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Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe	
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act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa	1572
Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln	
370 375 380	
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Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn	
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Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala	
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Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr	
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Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe	
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Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr	
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gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca	2100
Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr	
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ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag	2148

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Ser	Gln	Ser	Val	Ser	Gly	Glu	Glu	Ile	Asp	Ala	Met	Asp	Val	Gln	Gln		
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ctt	tca	caa	ata	gta	cca	aag	gtt	gca	gta	ttt	tac	aga	gct	agc	cca	2292	
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Arg	His	Lys	Met	Lys	Ile	Ile	Lys	Ser	Leu	Gln	Lys	Asn	Gly	Ser	Val		
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Val	Ala	Met	Thr	Gly	Asp	Gly	Val	Asn	Asp	Ala	Val	Ala	Leu	Lys	Ala		
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Ser	Ala	Ile	Glu	Glu	Gly	Lys	Gly	Ile	Tyr	Asn	Asn	Ile	Lys	Asn	Phe		
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Val	Arg	Phe	Gln	Leu	Ser	Thr	Ser	Ile	Ala	Ala	Leu	Thr	Leu	Ile	Ser		
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Val	Glu	Pro	Val	Asp	Lys	Asp	Val	Ile	Arg	Lys	Pro	Pro	Arg	Asn	Trp		
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 Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
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 Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
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aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964
 Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
 835 840 845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012
 Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro
 850 855 860

cgc ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060
 Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu
 865 870 875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108
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 880 885 890

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 Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser
 895 900 905 910

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 Ser Thr Ser Ser Ser Phe Leu Glu Val
 915

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Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser
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 Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly
 50 55 60
 Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr
 65 70 75 80
 Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn
 85 90 95
 Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met
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 Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr
 115 120 125
 Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys
 130 135 140
 Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe
 145 150 155 160
 Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln
 165 170 175
 Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala
 180 185 190
 Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys
 195 200 205
 Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile
 210 215 220
 Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly
 225 230 235 240
 Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser
 245 250 255
 Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val
 260 265 270
 Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu
 275 280 285
 Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys
 290 295 300
 Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile
 305 310 315 320
 Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr
 325 330 335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala
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 cccgccgtg cagcggtgac ccctccccg gctgccgcc tgcgccgcg ggtgaccccc 360
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 cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473
 Met Gly Ala Phe Leu Asp Lys Pro Lys Met
 1 5 10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta 521
 Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu
 15 20 25

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569
 Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala
 30 35 40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617
 Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val
 45 50 55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665
 Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His
 60 65 70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713
 Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly
 75 80 85 90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg	761
Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu	
95 100 105	
gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca	809
Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala	
110 115 120	
gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat	857
Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His	
125 130 135	
act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac	905
Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn	
140 145 150	
agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg	953
Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu	
155 160 165 170	
gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt	1001
Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg	
175 180 185	
gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac	1049
Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr	
190 195 200	
aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag	1097
Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu	
205 210 215	
cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att	1145
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile	
220 225 230	
atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc	1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu	
235 240 245 250	
tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa	1241
Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys	
255 260 265	
gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac	1289
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp	
270 275 280	
aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg	1337
Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser	
285 290 295	
cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc	1385
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys	
300 305 310	
aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta	1433

Arg Val Glu Glu Ile Lys Lys Gln Gly Glu Gly Val Phe Asp Leu
 315 320 325 330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481
 Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro
 335 340 345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529
 Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr
 350 355 360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577
 Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr
 365 370 375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629
 Asp Asp Met Trp
 380

aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatacctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaa at cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catattta at tatgaactgc tttaaatcac 1929

tatcaaagtt acaagaaatg ttgggcttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcatggt gtgtttggac ttgggggttg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtccc ttcatttaac tgtctttcag gatgttcctt cgttggttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

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Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu
 35 40 45
 Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val
 50 55 60
 Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg
 65 70 75 80
 Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn
 85 90 95
 Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
 100 105 110
 Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
 115 120 125
 Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
 130 135 140
 Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
 145 150 155 160
 Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
 165 170 175
 Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
 180 185 190
 Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
 195 200 205
 Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
 210 215 220
 Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
 225 230 235 240
 Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
 245 250 255
 Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln
 260 265 270
 Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr
 275 280 285
 Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln
 290 295 300
 Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly
 305 310 315 320
 Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro
 325 330 335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln
 340 345 350

Pro Gly Pro Gly Tyr Arg
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<210> 138
 <211> 1519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (11).. (1084)

<400> 138

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gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca      97
Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr
          15              20              25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata      145
Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile
          30              35              40              45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca      193
Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser
              50              55              60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa      241
Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys
              65              70              75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct      289
Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro
              80              85              90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag      337
Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
          95              100              105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca      385
Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
          110              115              120              125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa      433
Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
              130              135              140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca      481
Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
              145              150              155

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ccc agt gct cct gca gat cgt tca gga aca ccc gac aatt gct 529
 Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala
 160 165 170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577
 Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
 175 180 185

cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac 625
 Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
 190 195 200 205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673
 Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
 210 215 220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag 721
 Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
 225 230 235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca 769
 Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
 240 245 250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg 817
 Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
 255 260 265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa 865
 Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
 270 275 280 285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913
 Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
 290 295 300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961
 Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
 305 310 315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009
 Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
 320 325 330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc 1057
 Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly
 335 340 345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104
 Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
 350 355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164
 ttgaagaagt tcagaaattt aaaagcagag ctttttttat gatattcattg ttggtgttaa 1224
 ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta 1284

aaaatgtagc agcttctt ttacttttga acactactct tacatgtat agtgattga 1344
 cttagactttc tagcttccct tgtccggagg atattaaaat gctagggtga ggtttagcca 1404
 tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464
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<210> 139
 <211> 396
 <212> PRT
 <213> Homo sapiens

<400> 139

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Leu	Gly	Glu	Asp	Ile	Arg	Arg	Ile	Pro	Ile	His	Asn	Glu	Asp	Ile	Thr
			20					25					30		
Tyr	Asp	Glu	Leu	Val	Leu	Met	Met	Gln	Arg	Val	Phe	Arg	Gly	Lys	Leu
	35						40					45			
Leu	Ser	Asn	Asp	Glu	Val	Thr	Ile	Lys	Tyr	Lys	Asp	Glu	Asp	Gly	Asp
	50					55					60				
Leu	Ile	Thr	Ile	Phe	Asp	Ser	Ser	Asp	Leu	Ser	Phe	Ala	Ile	Gln	Cys
65				70					75					80	
Ser	Arg	Ile	Leu	Lys	Leu	Thr	Leu	Phe	Val	Asn	Gly	Gln	Pro	Arg	Pro
			85					90						95	
Leu	Glu	Ser	Ser	Gln	Val	Lys	Tyr	Leu	Arg	Arg	Glu	Leu	Ile	Glu	Leu
		100						105					110		
Arg	Asn	Lys	Val	Asn	Arg	Leu	Leu	Asp	Ser	Leu	Glu	Pro	Pro	Gly	Glu
	115					120						125			
Pro	Gly	Pro	Ser	Thr	Asn	Ile	Pro	Glu	Asn	Asp	Thr	Val	Asp	Gly	Arg
	130					135					140				
Glu	Glu	Lys	Ser	Ala	Ser	Asp	Ser	Ser	Gly	Lys	Gln	Ser	Thr	Gln	Val
145				150						155				160	
Met	Ala	Ala	Ser	Met	Ser	Ala	Phe	Asp	Pro	Leu	Lys	Asn	Gln	Asp	Glu
			165						170					175	
Ile	Asn	Lys	Asn	Val	Met	Ser	Ala	Phe	Gly	Leu	Thr	Asp	Asp	Gln	Val
		180						185					190		
Ser	Gly	Pro	Pro	Ser	Ala	Pro	Ala	Glu	Asp	Arg	Ser	Gly	Thr	Pro	Asp
		195				200						205			
Ser	Ile	Ala	Ser	Ser	Ser	Ser	Ala	Ala	His	Pro	Pro	Gly	Val	Gln	Pro
210						215					220				
Gln	Gln	Pro	Pro	Tyr	Thr	Gly	Ala	Gln	Thr	Gln	Ala	Gly	Gln	Met	Tyr

225

235

240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
 245 250 255
 Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
 260 265 270
 Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
 275 280 285
 Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
 290 295 300
 Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
 305 310 315 320
 Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
 325 330 335
 Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
 340 345 350
 Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
 355 360 365
 Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
 370 375 380
 Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
 385 390 395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19).. (1206)

<400> 140

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 Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu 10
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 atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99
 Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His 25
 15 20
 aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147
 Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val 40
 30 35
 ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195
 Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys 55
 45 50

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc	243
Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser	
60 65 70 75	
ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat	291
Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn	
80 85 90	
ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga	339
Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg	
95 100 105	
gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg	387
Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu	
110 115 120	
gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat	435
Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp	
125 130 135	
act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa	483
Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys	
140 145 150 155	
cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta	531
Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu	
160 165 170	
aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta	579
Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu	
175 180 185	
aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt	627
Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg	
190 195 200	
tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca	675
Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro	
205 210 215	
cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa	723
Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln	
220 225 230 235	
gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca	771
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala	
240 245 250	
cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag	819
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln	
255 260 265	
tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag	867
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln	
270 275 280	
ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc	915

Phe Gln Gly Tyr Gly Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
 285 290 295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963
 Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
 300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011
 Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
 320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059
 Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
 335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107
 Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro
 350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155
 Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg
 365 370 375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203
 Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr
 380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256
 Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

cattttttat gatattcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg 1496

atattaaaaat gctaggggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagatgattg aatcc 1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro
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Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr
 20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
 50 55 60
 Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
 65 70 75 80
 Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
 85 90 95
 Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
 100 105 110
 Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
 115 120 125
 His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
 130 135 140
 Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
 145 150 155 160
 Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
 165 170 175
 Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
 180 185 190
 Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
 195 200 205
 Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
 210 215 220
 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
 225 230 235 240
 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
 245 250 255
 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
 260 265 270
 Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
 275 280 285
 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
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 Val Gln Thr

<210> 142

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72).. (1040)

<400> 142

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gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110
      1          5          10
      Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158
Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu
      15          20          25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206
Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe
      30          35          40          45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254
Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His
      50          55          60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302
Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg
      65          70          75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe
      80          85          90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
      95          100          105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
      110          115          120          125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
      130          135          140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
      145          150          155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
      160          165          170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
      175          180          185

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gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca	686
Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro	
190 195 200 205	
tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg	734
Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg	
210 215 220	
ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac	782
Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn	
225 230 235	
ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac	830
Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn	
240 245 250	
tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc	878
Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val	
255 260 265	
cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc	926
Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu	
270 275 280 285	
aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg	974
Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu	
290 295 300	
agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag	1022
Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln	
305 310 315	
ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg	1070
Leu Thr His Val Gln Thr	
320	
ctgggggtgtg gggcagtctg ggtcctctca tcatccccac ttcccaggcc cagcctttcc	1130
aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tctgtcttct	1190
ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag	1250
cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg	1310
agaggggagg agtgggcagt gaagatgaag ccccatgctc agtcccctcc catccccac	1370
gcagctccac ccagtccca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc	1430
agcccctcct ctctgacctt taacctcact ctacacctgc accgtgcacc aacccttcac	1490
ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt	1550
ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt	1610
tggcac	1616

<400> 143
Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1 5 10 15
Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
20 25 30
Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45
Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60
Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80
Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95
Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His
100 105 110
Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe
115 120 125
Leu Gln Pro Leu Met His Cys Val
130 135

$\langle 220 \rangle$
 $\langle 221 \rangle$ CDS
 $\langle 222 \rangle$ (225) . . (632)

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ggcgcccttcc gtcccgttcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120
cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180
aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236
                                     Met Ala Gly Ala
                                     1
att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
ile ile Glu Asn Met Ser Thr Lys Lys Leu Cys ile Val Gly Gly ile
      5              10              15              20

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ctg ctc gtg ttc caa ctc atc gcc ttt ctg gtg gga ggc ttt att gct 332
 Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
 25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
 Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
 40 45 50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
 Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
 55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
 Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
 70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
 Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
 85 90 95 100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572
 Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser
 105 110 115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620
 Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu
 120 125 130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672
 Met His Cys Val
 135

ttgttaatta gtgacatagt aacatctgta gcagctgggt agtaaacctc atgtgggggt 732
 ggggtggggg tgtattcctt ggggatgggt ttgggccgaa tggggagtgg aatatttgac 792
 atttttcctg ttttaaattc taggatagat tttaacatcc ttgcggtcc cagtccaagg 852
 taggctgggtg tcatagtctt ctactccta atccatgacc actgtttttt tcctatttat 912
 atcaccaggt agcctactga gttaatatatt aagttgtcaa tagataagtg tccctgtttt 972
 gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032
 gaaaccaa at ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092
 ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152
 tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212
 gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 145
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 Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe
 20 25 30
 Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln
 35 40 45
 Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg
 50 55 60
 Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
 65 70 75 80
 Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
 85 90 95
 Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser
 100 105 110
 Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
 115 120 125
 Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
 130 135 140
 Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
 145 150 155 160
 Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
 165 170 175
 Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
 180 185 190
 Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
 195 200 205
 Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
 210 215 220
 Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
 225 230 235 240
 Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
 245 250 255
 Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
 260 265 270
 Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
 275 280 285
 Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
 290 295 300

Ile Ile Val Ala Gly Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
 305 310 315 320
 Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
 325 330 335
 Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
 340 345 350
 Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
 355 360 365
 Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
 370 375 380
 Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
 385 390 395 400
 Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
 405 410 415
 Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
 420 425 430
 Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
 435 440 445
 Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
 450 455 460
 Ala Ser Gly Ile
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<210> 146
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 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (379).. (1782)

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 cccagaaaagg aggcgaggaa ggaggagtg tgtgagagga gggagcaaaa agctcaccct 180
 aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240
 tagaaaacat gaggaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300
 tcatgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360
 tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411
 Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag	459
Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys	
15 20 25	
agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc	507
Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe	
30 35 40	
aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt	555
Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val	
45 50 55	
tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc	603
Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala	
60 65 70 75	
cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag	651
His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys	
80 85 90	
act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc	699
Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe	
95 100 105	
atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg	747
Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg	
110 115 120	
ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata	795
Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile	
125 130 135	
aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag	843
Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys	
140 145 150 155	
gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att	891
Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile	
160 165 170	
atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg	939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val	
175 180 185	
ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc	987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile	
190 195 200	
aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg	1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met	
205 210 215	
ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg	1083
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu	
220 225 230 235	

tcc ttc tgg atc att ttc tgt ggc gag cac atg atg gat ccc cac gag Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu	1131
240 245 250	
cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val	1179
255 260 265	
ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln	1227
270 275 280	
ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu	1275
285 290 295	
ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr	1323
300 305 310 315	
ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser	1371
320 325 330	
ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His	1419
335 340 345	
tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu	1467
350 355 360	
gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr	1515
365 370 375	
gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala	1563
380 385 390 395	
ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu	1611
400 405 410	
atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser	1659
415 420 425	
aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe	1707
430 435 440	
gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe	1755
445 450 455	
atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca Ile Asn Asp Asn Ala Ala Ser Gly Ile	1802

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862
 acaaatacac tcatttagcc tttatctcaa aatgttaaata ataaggaaaa aagcgtcaac 1922
 aataaatatt ctttgagtat t 1943

<210> 147
 <211> 460
 <212> PRT
 <213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
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Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly
 20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
 35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
 50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
 65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
 85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
 100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
 115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
 130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
 145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
 165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
 180 185 190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
 195 200 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
 210 215 220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp

225

230

235

240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
260 265 270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
275 280 285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
290 295 300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg
305 310 315 320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg
325 330 335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu
340 345 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser
355 360 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val
370 375 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val
385 390 395 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
405 410 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
420 425 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
435 440 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
450 455 460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376).. (1755)

<400> 148

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gccttcgctc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180
 acattttatt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240
 aaaacatgag caccaagaag ctgtgcattg ttgggtgggat tctgctcgtg ttccaaatca 300
 tcgcctttct ggtgggaggc ttgattgctc cagggccac aacggcagtg tcctacatgt 360
 cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411
 Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser
 1 5 10
 tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459
 Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg
 15 20 25
 caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507
 Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr
 30 35 40
 ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555
 Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe
 45 50 55 60
 gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603
 Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys
 65 70 75
 tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651
 Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr
 80 85 90
 gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699
 Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys
 95 100 105
 ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747
 Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
 110 115 120
 aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795
 Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
 125 130 135 140
 caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843
 Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
 145 150 155
 acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891
 Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
 160 165 170
 atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939
 Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
 175 180 185
 ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987

Gly	Ile	Ser	Met	Thr	Phe	Ile	Asn	Ile	Pro	Val	Glu	Trp	Phe	Ser	Ile	
190						195					200					
ggg	ttt	gac	tgg	acc	tgg	atg	ctg	ctg	ttt	ggg	gac	atc	cga	cag	ggc	1035
Gly	Phe	Asp	Trp	Thr	Trp	Met	Leu	Leu	Phe	Gly	Asp	Ile	Arg	Gln	Gly	
205					210					215					220	
atc	ttc	tat	gcg	atg	ctt	ctg	tcc	ttc	tgg	atc	atc	ttc	tgt	ggc	gag	1083
Ile	Phe	Tyr	Ala	Met	Leu	Leu	Ser	Phe	Trp	Ile	Ile	Phe	Cys	Gly	Glu	
				225					230					235		
cac	atg	atg	gat	cag	cac	gag	cgg	aac	cac	atc	gca	ggg	tat	tgg	aag	1131
His	Met	Met	Asp	Gln	His	Glu	Arg	Asn	His	Ile	Ala	Gly	Tyr	Trp	Lys	
			240					245					250			
caa	gtc	gga	ccc	att	gcc	gtt	ggc	tcc	ttc	tgc	ctc	ttc	ata	ttt	gac	1179
Gln	Val	Gly	Pro	Ile	Ala	Val	Gly	Ser	Phe	Cys	Leu	Phe	Ile	Phe	Asp	
		255					260					265				
atg	tgt	gag	aga	ggg	gta	caa	ctc	acg	aat	ccc	ttc	tac	agt	atc	tgg	1227
Met	Cys	Glu	Arg	Gly	Val	Gln	Leu	Thr	Asn	Pro	Phe	Tyr	Ser	Ile	Trp	
	270					275					280					
act	aca	gac	att	gga	aca	gag	ctg	gcc	atg	gcc	ttc	atc	atc	gtg	gct	1275
Thr	Thr	Asp	Ile	Gly	Thr	Glu	Leu	Ala	Met	Ala	Phe	Ile	Ile	Val	Ala	
285					290					295					300	
gga	atc	tgc	ctc	tgc	ctc	tac	ttc	ctg	ttt	cta	tgc	ttc	atg	gta	ttt	1323
Gly	Ile	Cys	Leu	Cys	Leu	Tyr	Phe	Leu	Phe	Leu	Cys	Phe	Met	Val	Phe	
				305					310					315		
cag	gtg	ttt	cgg	aac	atc	agt	ggg	aag	cag	tcc	agc	ctg	cca	gct	atg	1371
Gln	Val	Phe	Arg	Asn	Ile	Ser	Gly	Lys	Gln	Ser	Ser	Leu	Pro	Ala	Met	
			320					325					330			
agc	aaa	gtc	cgg	cgg	cta	cac	tat	gag	ggg	cta	att	ttt	agg	ttc	aag	1419
Ser	Lys	Val	Arg	Arg	Leu	His	Tyr	Glu	Gly	Leu	Ile	Phe	Arg	Phe	Lys	
		335					340					345				
ttc	ctc	atg	ctt	atc	acc	ttg	gcc	tgc	gct	gcc	atg	act	gtc	atc	ttc	1467
Phe	Leu	Met	Leu	Ile	Thr	Leu	Ala	Cys	Ala	Ala	Met	Thr	Val	Ile	Phe	
		350				355					360					
ttc	atc	gtt	agt	cag	gta	acg	gaa	ggc	cat	tgg	aaa	tgg	ggc	ggc	atc	1515
Phe	Ile	Val	Ser	Gln	Val	Thr	Glu	Gly	His	Trp	Lys	Trp	Gly	Gly	Ile	
365					370					375					380	
aca	gtc	caa	gtg	aac	agt	gcc	ttt	ttc	aca	ggc	atc	tat	ggg	atg	tgg	1563
Thr	Val	Gln	Val	Asn	Ser	Ala	Phe	Phe	Thr	Gly	Ile	Tyr	Gly	Met	Trp	
				385					390					395		
aat	ctg	tat	gtc	ttt	gct	ctg	atg	ttc	ttg	tat	gca	cca	tcc	cat	aaa	1611
Asn	Leu	Tyr	Val	Phe	Ala	Leu	Met	Phe	Leu	Tyr	Ala	Pro	Ser	His	Lys	
			400					405					410			
aac	tat	gga	gaa	gac	cag	tcc	aat	gga	atg	caa	ctc	cca	tgt	aaa	tcg	1659
Asn	Tyr	Gly	Glu	Asp	Gln	Ser	Asn	Gly	Met	Gln	Leu	Pro	Cys	Lys	Ser	
		415					420					425				

agg gaa gat tgt gct ttg ttt gtt tgc gaa ctt tat caa gaa ttg ttc 1707
 Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
 430 435 440

agc gct tgc aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755
 Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
 445 450 455 460

tgagtcaaca aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaat 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc 1919

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<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
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 20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
 130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
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Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175

Asp Arg His Lys Met Leu Ser
 180

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<220>
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 atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1 5 10 15
 cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30
 tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45
 tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60
 cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80
 gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95
 tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110
 gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125
 gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
 130 135 140
 ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160
 cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698
 Asp Arg His Lys Met Leu Ser

180

ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 758
 tcggttccag tcttcccttt aaaagcctgt ggcatTTTTc ctcttctcc ctaactttag 818
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 aagctggtgt tcgctgtccc ctgtgcactt ctgcactgg ggcatggagt gcccatgcat 1298
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 atctgaacac cacagcccct gtacttgggt tgcctcttgt cctgaactt cgttgtacca 1478
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 <212> DNA
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<220>
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 aggctgtcgg ttcggaacat gtctccacc accccaccct ctgtggctcc aggcttcatt 180
 ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230
 Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly
 1 5 10
 att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278
 Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys

ctg	ggg	agt	ctg	tgt	tca	ggc	agc	cag	gag	tca	aag	ctt	ctc	cat	gcc	326
Leu	Gly	Ser	Leu	Cys	Ser	Gly	Ser	Gln	Glu	Ser	Lys	Leu	Leu	His	Ala	
30					35				40						45	
atg	gta	ctc	ctg	gct	ctg	ggc	cag	gac	acg	gag	gcc	agg	gtc	tct	ctg	374
Met	Val	Leu	Leu	Ala	Leu	Gly	Gln	Asp	Thr	Glu	Ala	Arg	Val	Ser	Leu	
				50					55					60		
gag	tcc	ttg	aag	atg	aac	aca	gta	gcc	cag	ctg	gta	gcc	cac	cag	tgg	422
Glu	Ser	Leu	Lys	Met	Asn	Thr	Val	Ala	Gln	Leu	Val	Ala	His	Gln	Trp	
			65					70					75			
gca	gac	atg	gag	acc	aca	gag	ggc	cct	gag	gag	cct	cca	gac	ttg	tcc	470
Ala	Asp	Met	Glu	Thr	Thr	Glu	Gly	Pro	Glu	Glu	Pro	Pro	Asp	Leu	Ser	
		80					85					90				
tgg	acg	gtg	gct	cgc	ctg	tac	cac	ctg	ctg	gct	gag	gag	aac	ctg	tgt	518
Trp	Thr	Val	Ala	Arg	Leu	Tyr	His	Leu	Leu	Ala	Glu	Glu	Asn	Leu	Cys	
	95					100					105					
ccg	gcc	tct	aca	agg	gac	atg	gct	tac	cag	gtg	gcc	ctt	cgt	gac	ttt	566
Pro	Ala	Ser	Thr	Arg	Asp	Met	Ala	Tyr	Gln	Val	Ala	Leu	Arg	Asp	Phe	
110					115				120						125	
gcc	tcc	cag	ggt	gac	cac	cag	ctg	ggc	caa	ctc	cag	aat	gag	gcc	tgg	614
Ala	Ser	Gln	Gly	Asp	His	Gln	Leu	Gly	Gln	Leu	Gln	Asn	Glu	Ala	Trp	
				130				135						140		
gat	cgg	tgc	agt	tca	gat	atc	aag	ggg	gac	ccc	agt	ggt	ttc	cag	cca	662
Asp	Arg	Cys	Ser	Ser	Asp	Ile	Lys	Gly	Asp	Pro	Ser	Gly	Phe	Gln	Pro	
			145					150					155			
ctc	cat	tct	cat	cag	ggt	tcc	ctg	cag	cca	cct	tca	gca	tcc	cct	gca	710
Leu	His	Ser	His	Gln	Gly	Ser	Leu	Gln	Pro	Pro	Ser	Ala	Ser	Pro	Ala	
		160					165					170				
gtg	acc	aga	agc	cag	cct	cgt	ccc	att	gac	aca	cca	gac	tgg	agt	tgg	758
Val	Thr	Arg	Ser	Gln	Pro	Arg	Pro	Ile	Asp	Thr	Pro	Asp	Trp	Ser	Trp	
	175					180					185					
gga	cat	acg	tta	cac	tcc	acc	aac	agc	act	gcc	tca	ctg	gcc	agc	cac	806
Gly	His	Thr	Leu	His	Ser	Thr	Asn	Ser	Thr	Ala	Ser	Leu	Ala	Ser	His	
190					195					200					205	
cta	gag	atc	agc	cag	tca	ccc	act	ctt	gcc	ttt	ctc	tct	tca	cac	cat	854
Leu	Glu	Ile	Ser	Gln	Ser	Pro	Thr	Leu	Ala	Phe	Leu	Ser	Ser	His	His	
				210					215					220		
gga	acc	cat	ggg	ccc	agc	aag	cta	tgt	aac	aca	ccg	ctg	gac	act	cag	902
Gly	Thr	His	Gly	Pro	Ser	Lys	Leu	Cys	Asn	Thr	Pro	Leu	Asp	Thr	Gln	
			225					230					235			
gag	cct	cag	ctt	gtc	cct	gaa	ggc	tgc	caa	gaa	cct	gag	gag	ata	agc	950
Glu	Pro	Gln	Leu	Val	Pro	Glu	Gly	Cys	Gln	Glu	Pro	Glu	Glu	Ile	Ser	
		240					245					250				

tgg cct cca tca gtg g acc agt gtc tcc tta ggg tta c cac gaa	998
Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu	
255 260 265	
att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct	1046
Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro	
270 275 280 285	
gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc	1094
Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys	
290 295 300	
aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa	1142
Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu	
305 310 315	
agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt	1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val	
320 325 330	
cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct	1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro	
335 340 345	
gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct	1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro	
350 355 360 365	
ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc	1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser	
370 375 380	
aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat	1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr	
385 390 395	
aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt	1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg	
400 405 410	
att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc	1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe	
415 420 425	
tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa	1526
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln	
430 435 440 445	
gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc	1574
Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser	
450 455 460	
ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac	1622
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn	
465 470 475	
agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca	1670
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro	

ctt	gag	tgt	tcc	cag	gcc	cag	ctc	agc	cca	gat	aca	acc	aga	ctg	ctc	1718
Leu	Glu	Cys	Ser	Gln	Ala	Gln	Leu	Ser	Pro	Asp	Thr	Thr	Arg	Leu	Leu	
495						500					505					
cac	agc	att	gtg	tgg	ctg	gat	gaa	cac	tcc	cca	atc	ttc	gcc	aga	aag	1766
His	Ser	Ile	Val	Trp	Leu	Asp	Glu	His	Ser	Pro	Ile	Phe	Ala	Arg	Lys	
510					515					520					525	
gtg	gca	aac	acc	ttc	aag	aca	cag	aag	ctc	cag	gca	cag	cgg	gta	cgc	1814
Val	Ala	Asn	Thr	Phe	Lys	Thr	Gln	Lys	Leu	Gln	Ala	Gln	Arg	Val	Arg	
				530					535					540		
tgg	aag	aaa	gcg	cag	gag	gcc	aga	acc	ctc	aag	gag	cag	agc	ata	cag	1862
Trp	Lys	Lys	Ala	Gln	Glu	Ala	Arg	Thr	Leu	Lys	Glu	Gln	Ser	Ile	Gln	
			545					550					555			
ctg	gag	gca	gag	cgg	caa	aac	gtg	gca	gcc	ata	tct	gct	gcc	tac	aca	1910
Leu	Glu	Ala	Glu	Arg	Gln	Asn	Val	Ala	Ala	Ile	Ser	Ala	Ala	Tyr	Thr	
		560					565					570				
gcc	tat	gtc	cat	agc	tat	agg	gcc	tgg	caa	gca	gag	atg	aac	aaa	ctt	1958
Ala	Tyr	Val	His	Ser	Tyr	Arg	Ala	Trp	Gln	Ala	Glu	Met	Asn	Lys	Leu	
	575					580					585					
ggg	gtg	gct	ttt	ggg	aag	aac	ttg	tca	ctg	ggg	act	cca	aca	ccc	agc	2006
Gly	Val	Ala	Phe	Gly	Lys	Asn	Leu	Ser	Leu	Gly	Thr	Pro	Thr	Pro	Ser	
590					595					600					605	
tgg	ccc	gga	tgt	cca	cag	cca	ata	cct	tct	cat	cct	cag	ggt	ggt	act	2054
Trp	Pro	Gly	Cys	Pro	Gln	Pro	Ile	Pro	Ser	His	Pro	Gln	Gly	Gly	Thr	
				610					615					620		
cca	gtt	ttc	ccc	tat	tcc	cca	cag	cct	cca	tcc	ttc	cct	cag	cct	cca	2102
Pro	Val	Phe	Pro	Tyr	Ser	Pro	Gln	Pro	Pro	Ser	Phe	Pro	Gln	Pro	Pro	
			625					630					635			
tgc	ttc	cct	cag	cct	cca	tcc	ttc	cct	cag	cct	cca	tcc	ttc	cca	ctg	2150
Cys	Phe	Pro	Gln	Pro	Pro	Ser	Phe	Pro	Gln	Pro	Pro	Ser	Phe	Pro	Leu	
		640					645					650				
cct	cca	gtc	tct	tcc	cca	cag	tcc	caa	tcc	ttt	cca	tca	gcc	tcc	tcc	2198
Pro	Pro	Val	Ser	Ser	Pro	Gln	Ser	Gln	Ser	Phe	Pro	Ser	Ala	Ser	Ser	
	655					660					665					
cca	gcc	cca	cag	act	cca	gga	cct	cag	cct	ctc	att	att	cac	cat	gcc	2246
Pro	Ala	Pro	Gln	Thr	Pro	Gly	Pro	Gln	Pro	Leu	Ile	Ile	His	His	Ala	
670					675					680					685	
cag	atg	gtt	cag	ctg	ggt	gtc	aac	aat	cac	atg	tgg	ggc	cac	aca	ggg	2294
Gln	Met	Val	Gln	Leu	Gly	Val	Asn	Asn	His	Met	Trp	Gly	His	Thr	Gly	
				690					695					700		
gcc	cag	tca	tct	gat	gac	aag	act	gag	tgt	tcg	gag	aac	ccc	tgt	atg	2342
Ala	Gln	Ser	Ser	Asp	Asp	Lys	Thr	Glu	Cys	Ser	Glu	Asn	Pro	Cys	Met	
			705					710					715			

ggc cct ctg act ga ag ggc gaa ccc ctt ctt gag act gag 2387
 Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
 720 725 730

tgaccagggtt ggaccccacc tagatggcta gagtgacaag attggacttc acctgggtcc 2447
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<210> 152
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 <212> PRT
 <213> Homo sapiens

<400> 152

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 20 25 30
 Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu
 35 40 45
 Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu
 50 55 60
 Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met
 65 70 75 80
 Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val
 85 90 95
 Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser
 100 105 110
 Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln
 115 120 125
 Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys
 130 135 140
 Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser
 145 150 155 160
 His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr
 180 185 190
 Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile
 195 200 205
 Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His
 210 215 220
 Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln
 225 230 235 240
 Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro
 245 250 255
 Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val
 260 265 270
 Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu
 275 280 285
 Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu
 290 295 300
 Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly
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 Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val
 385 390 395 400
 Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu
 405 410 415
 Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu
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 Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile
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 Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr
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Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys
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 Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile
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 Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn
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 Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
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 Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
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 Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
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 Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
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 675 680 685
 Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser
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Met Ala Cys Thr Gly Pro
1 5
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Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys
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ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210
Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln
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ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258
Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu
40 45 50
act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306
Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala
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cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354
Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro
75 80 85
gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402
Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu
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Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr
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Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly
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Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly
135 140 145 150
gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca 594
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Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly
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gaa Glu	acc Thr	agc Ser	acc Thr	aac Asn	tac Tyr	295	cca Pro	gtg Val	gag Glu	tgc Cys	acc Thr	300	gag Glu	ggg Gly	tct Ser	gca Ala	ggc Gly	1026
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tct Ser	gtc Val	aaa Lys	gac Asp	cag Gln	acg Thr	330	cca Pro	ctc Leu	caa Gln	ctt Leu	tct Ser	335	gta Val	gaa Glu	gat Asp	acc Thr	acc Thr	1122
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cac His	atc Ile	gcc Ala	ctg Leu	cgg Arg	gtt Val	410	cgg Arg	gag Glu	aag Lys	ctg Leu	gag Glu	415	gcc Ala	ctt Leu	ggc Gly	gtg Val	ccc Pro	1362
gac Asp	ggg Gly	gcc Ala	acc Thr	ttc Phe	tgc Cys	425	gag Glu	gat Asp	ttc Phe	cag Gln	gtg Val	430	ccg Pro	ggg Gly	cgc Arg	ggg Gly	gag Glu	1410

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu 440 445 450	1458
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caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val 475 480 485	1554
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acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln 505 510 515	1650
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gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg 535 540 545 550	1746
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Phe Pro Thr Ala Ser Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro
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ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178
 Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His
 680 685 690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226
 Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
 695 700 705 710

gca gaa tgaccgctg tccttgccctg accacctggg gaacaccct ggaccaggc 2282
 Ala Glu

atcgccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat 2342

gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaacgggc 2402

gcgatgatgc cctggctttc aggggtgtca gaactggata cggtgtttac aattccaatc 2462

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<211> 712

<212> PRT

<213> Homo sapiens

<400> 154

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 35 40 45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu
 50 55 60



Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
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Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
 85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
 100 105 110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
 115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
 130 135 140

Gly Trp Asp Ile Ala  Tyr Asp Pro Gly Ser Ile Arg Thr Leu  Gln Ser
 145 150 155 160
 Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
 165 170 175
 Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
 180 185 190
 Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
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 Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
 210 215 220
 His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
 225 230 235 240
 Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
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 Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro
 260 265 270
 Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
 275 280 285
 Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
 290 295 300
 Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
 305 310 315 320
 Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu
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 Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
 340 345 350
 Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser
 355 360 365
 Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
 370 375 380
 Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
 385 390 395 400
 His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
 405 410 415
 Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
 420 425 430
 Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
 435 440 445
 Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu

450

455

460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
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 Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
 485 490 495
 Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
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 Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
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 Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
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 Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
 545 550 555 560
 Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
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 Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
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 Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
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 Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
 660 665 670
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<213> Homo sapiens

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<400> 155

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Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu
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Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu
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Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala
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Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp
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Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro
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Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp
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atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg 631
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly
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gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct 679
Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser
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ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag 727
Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys
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aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc 775
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser
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185 200	190 210
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205	210
gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu	967
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230	235 240 245
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250	255 260
cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu	1111
265	270 275
tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile	1159
280	285 290
ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala	1207
295	300 305
ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly	1255
310	315 320 325
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345	350 355
ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu	1399
360	365 370
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Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln	
425 430 435	
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Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala	
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Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys	
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Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro	
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Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu	
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Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile	
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Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp	
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Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val	
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Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala	
585 590 595	
cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag	2119
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu	
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Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu	
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630

640

645

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ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr	2455
ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro	2503
atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser	2551
cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu	2599
agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu	2647
cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser	2695
cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg	2743
act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly	2791
gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly	2839
gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly	2887

gcc tct ccc agg gtc ag cct gag ccc cca cca ggg gtc t gcc cag 2935
 Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln
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cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg 2983
 His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu
 890 895 900

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Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro
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Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg
 85 90 95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met
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Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr
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Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr

130

135

140

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 Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
 195 200 205
 Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp
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 Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln
 225 230 235 240
 Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser
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 Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu
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 Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp
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 325 330 335
 Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met
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 Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr
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 Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser
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 Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val
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 Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser
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 Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala
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 Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu
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 Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
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 Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
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 Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser
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Pro Arg Val Pro Ser o Pro Pro Ser Pro Arg Leu Arg Arg Thr
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 Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser
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 Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr
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 Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser
 820 825 830
 Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val
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 Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly
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 cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc 172
 Met His Tyr Asp Gly His Val
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 cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc 220
 Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser
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 Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu
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gag gag gag gag agc cct gtg gat ggc aaa ggg gac cgg aag agc aca	316
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Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp	
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Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile	
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Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val	
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ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac	508
Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp	
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Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala	
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Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe	
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Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr	

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gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His 315 320 325	1132
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Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr	
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acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc 3148
 Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser
 985 990 995

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Thr	Gly	Pro	Pro 180	Ala	Leu	Glu	Arg	Val 185	Asp	Ala	Gln	Ser	Arg	Arg	Glu 190
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Phe 210	Leu	Gly	Glu	Ala	Ser	Ile 215	Pro	Gly	Gln	Glu	Pro 220	Pro	Thr	Pro	Ser
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Ser	Trp	Lys	Asn	Arg 245	Ala	Ala	Ser	Arg	Phe 250	Ser	Gly	Phe	Phe	Ser	Ser 255
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Leu 370	Gln	Glu	Ser	Gly	Leu	Leu 375	Cys	Glu	Val	Glu	Ala 380	Glu	Arg	Leu	Phe
Ser 385	Asn	Ile	Pro	Glu	Ile 390	Ala	Gln	Leu	His	Arg 395	Arg	Leu	Trp	Ala	Ser 400
Val	Met	Ala	Pro 405	Val	Leu	Glu	Lys	Ala	Arg 410	Arg	Thr	Arg	Ala	Leu	Leu 415
Gln	Pro	Gly	Asp 420	Phe	Leu	Lys	Gly	Phe	Lys 425	Met	Phe	Gly	Ser	Leu	Phe 430
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Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
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 Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
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 940 945 950

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Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
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745

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Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
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Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
      105           110           115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
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Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala			
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895

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 agtgggcccc aggaatgtgt ttccttctct ccaccatgtt tttatagctc ttgggctggg 3919
 agaagaggcg ggtctgggtc tttgtttctg agctttgttc tatgttctc catgctacgg 3979
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 35 40 45
 Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
 50 55 60
 Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
85 90 95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
130 135 140

Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu
145 150 155 160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
165 170 175

Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
195 200 205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
245 250 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp
260 265 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
275 280 285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
290 295 300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305 310 315 320

Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
325 330 335

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala
340 345 350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser
355 360 365

Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser
370 375 380

Tyr	Gln	Gly	His	Asp	Gln	Phe	Lys	Arg	Arg	Leu	Pro	Ser	Gly	Gln	Met	385	390	395	400
Arg	Gln	Leu	Cys	Ile	Ala	Met	Asp	Arg	Ser	Phe	Asp	Ala	Val	Gly	Pro	405	410	415	
Arg	Pro	Arg	Leu	Asp	Ser	Met	Ser	Ser	Val	Glu	Glu	Asp	Asp	Tyr	Asp	420	425	430	
Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys	Asn	Val	Ile	Arg	Thr	Lys	Gln	435	440	445	
Tyr	Leu	Cys	Val	Ala	Asp	Leu	Ala	Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	450	455	460	
Lys	Lys	Tyr	Gln	Ile	Tyr	Phe	Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	465	470	475	480
Tyr	Ala	Leu	Pro	Val	Val	Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	485	490	495	
Asn	Val	Thr	Gly	Asn	Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	500	505	510	
His	Pro	Leu	Gly	Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	515	520	525	
Gly	Tyr	Ile	Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	530	535	540	
Glu	Ile	Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Tyr	Ala	Leu	545	550	555	560
Glu	Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr	565	570	575	
Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys	Pro	580	585	590	
Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met	Ile	Ala	595	600	605	
Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro	Asp	Ile	Asn	610	615	620	
Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile	Val	Ile	Phe	Phe	625	630	635	640
Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	Thr	Ala	Phe	Trp	Ile	645	650	655	
Val	Phe	Ser	Val	Ile	His	Ile	Ile	Ser	Thr	Leu	Leu	Leu	Ser	Thr	Gln	660	665	670	
Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	Asp	Phe	Gly	Ile	Phe	Arg	Arg	675	680	685	

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
 690 695 700
 Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
 705 710 715 720
 Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
 725 730 735
 Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
 740 745 750
 Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
 755 760 765
 Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
 770 775 780
 Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
 785 790 795 800
 Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
 805 810 815
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
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 Lys Ile Tyr Val Phe
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 Met Phe Ala Leu Gly Leu Pro Phe Leu Val
 1 5 10
 ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag 161
 Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys
 15 20 25
 aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag 209
 Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu
 30 35 40

gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc	257
Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr	
45 50 55	
cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag	305
Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys	
60 65 70	
cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg	353
Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val	
75 80 85 90	
gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag	401
Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys	
95 100 105	
tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag	449
Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys	
110 115 120	
aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca	497
Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser	
125 130 135	
cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt	545
Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe	
140 145 150	
gtg ctc agg act ggg gag cag ttc agc ttc aat acc aca gca gca cag	593
Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln	
155 160 165 170	
ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att	641
Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile	
175 180 185	
gtc aag gtg acc tcc aac aag gcc ttc ccc tgc tca gtc atc tcc att	689
Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile	
190 195 200	
cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc	737
Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe	
205 210 215	
atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag	785
Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln	
220 225 230	
cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag	833
Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys	
235 240 245 250	
acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca	881
Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala	
255 260 265	
gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg	929

Glu	Asp	Glu	Pro	Val	Leu	Gln	Gly	His	Arg	Gln	Lys	Thr	Ser	Val		
270							275						280			
ctg	gtg	tct	caa	gca	gtc	acg	tct	gag	gca	tac	gtc	agt	ggg	atg	ctc	977
Leu	Val	Ser	Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	
	285						290					295				
ttt	tgc	ctg	ggg	ata	ttt	ctc	tcc	ttt	tac	ctg	ctg	acc	gtc	ctc	ctg	1025
Phe	Cys	Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	
	300					305					310					
gcc	tgc	tgg	gag	aac	tgg	agg	cag	aag	aag	aag	acc	ctg	ctg	gtg	gcc	1073
Ala	Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala	
	315				320				325						330	
att	gac	cga	gcc	tgc	cca	gaa	agc	ggg	cac	cct	cga	gtc	ctg	gct	gat	1121
Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Pro	Arg	Val	Leu	Ala	Asp	
			335						340					345		
tct	ttt	cct	ggc	agt	tcc	cct	tat	gag	ggg	tac	aac	tat	ggc	tcc	ttt	1169
Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly	Ser	Phe	
			350						355					360		
gag	aat	gtt	tct	gga	tct	acc	gat	ggg	ctg	gtt	gac	agc	gct	ggc	act	1217
Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser	Ala	Gly	Thr	
	365						370					375				
ggg	gac	ctc	tct	tac	ggg	tac	cag	ggg	cac	gac	cag	ttc	aag	cgg	cgc	1265
Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	His	Asp	Gln	Phe	Lys	Arg	Arg	
	380					385					390					
ctc	ccc	tct	ggc	cag	atg	cgg	cag	ctg	tgc	att	gcc	atg	ggc	cgc	tcc	1313
Leu	Pro	Ser	Gly	Gln	Met	Arg	Gln	Leu	Cys	Ile	Ala	Met	Gly	Arg	Ser	
	395				400					405					410	
ttt	gaa	cct	gta	ggg	act	cgg	ccc	cga	gtg	gac	tcc	atg	agc	tct	gtg	1361
Phe	Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val	
			415						420					425		
gag	gag	gat	gac	tac	gac	aca	ttg	acc	gac	atc	gat	tcc	gac	aag	aat	1409
Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys	Asn	
			430					435					440			
gtc	att	cgc	acc	aag	caa	tac	ctc	tat	gtg	gct	gac	ctg	gca	cgg	aag	1457
Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala	Arg	Lys	
	445						450					455				
gac	aag	cgt	gtt	ctg	cgg	aaa	aag	tac	cag	atc	tac	ttc	tgg	aac	att	1505
Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe	Trp	Asn	Ile	
	460					465					470					
gcc	acc	att	gct	gtc	ttc	tat	gcc	ctt	cct	gtg	gtg	cag	ctg	gtg	atc	1553
Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val	Gln	Leu	Val	Ile	
	475				480					485					490	
acc	tac	cag	acg	gtg	gtg	aat	gtc	aca	ggg	aat	cag	gac	atc	tgc	tac	1601
Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn	Gln	Asp	Ile	Cys	Tyr	
			495						500					505		

tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac	1649
Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn	
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aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg	1697
Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu	
525 530 535	
ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc	1745
Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg	
540 545 550	
aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt	1793
Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu	
555 560 565 570	
ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct	1841
Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala	
575 580 585	
tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg	1889
Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser	
590 595 600	
ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag	1937
Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys	
605 610 615	
cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg	1985
Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu	
620 625 630	
gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg	2033
Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly	
635 640 645 650	
aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc	2081
Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr	
655 660 665	
ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac	2129
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp	
670 675 680	
tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc	2177
Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile	
685 690 695	
cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc	2225
Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val	
700 705 710	
atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg	2273
Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met	
715 720 725 730	
cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac	2321

Arg Pro Asn Asp Phe Ser Tyr Leu Leu Ala Ile Gly Cys Asn
 735 740 745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369
 Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly
 750 755 760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417
 Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val
 765 770 775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465
 Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp
 780 785 790

cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc 2513
 Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu
 795 800 805 810

ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc 2561
 Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile
 815 820 825

gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg 2609
 Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly
 830 835 840

tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg 2658
 Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly
 845 850 855

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<211> 855

<212> PRT

<213> Homo sapiens

<400> 166

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Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val
 35 40 45
 Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
 50 55 60
 Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
 65 70 75 80
 Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
 85 90 95
 Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
 100 105 110
 Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
 115 120 125
 Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
 130 135 140
 Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
 145 150 155 160
 Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
 165 170 175
 Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
 180 185 190
 Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
 195 200 205
 Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
 210 215 220
 Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 225 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
 245 250 255
 Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp
 260 265 270
 Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
 275 280 285
 Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
 290 295 300
 Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
 305 310 315 320
 Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
 325 330 335

Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser
 340 345 350
 Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser
 355 360 365
 Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly
 370 375 380
 Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
 385 390 395 400
 Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
 405 410 415
 Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
 420 425 430
 Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
 435 440 445
 Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
 450 455 460
 Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
 465 470 475 480
 Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
 485 490 495
 Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
 500 505 510
 His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
 515 520 525
 Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
 530 535 540
 Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu
 545 550 555 560
 Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
 565 570 575
 Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
 580 585 590
 Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
 595 600 605
 Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
 610 615 620
 Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
 625 630 635 640

Ser Val Leu Gly Val Phe Gly Lys Gly Asn Thr Ala Trp Ile
 645 650 655
 Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln
 660 665 670
 Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg
 675 680 685
 Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
 690 695 700
 Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn
 705 710 715 720
 Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
 725 730 735
 Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
 740 745 750
 Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
 755 760 765
 Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
 770 775 780
 Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
 785 790 795 800
 Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
 805 810 815
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
 820 825 830
 Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser
 835 840 845
 Ser Cys Leu Leu Pro Cys Gly
 850 855

<210> 167
 <211> 2815
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (56).. (571)

<400> 167
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agg cgc cag cct gca ggt ggc ggc ctg ctg ctc ggg ctc ttg	106
Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu	
5 10 15	
gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat	154
Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr	
20 25 30	
cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg	202
Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg	
35 40 45	
tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc	250
Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe	
50 55 60 65	
ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc	298
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile	
70 75 80	
cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat	346
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn	
85 90 95	
gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag	394
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln	
100 105 110	
ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct	442
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro	
115 120 125	
gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc	490
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro	
130 135 140 145	
cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct	538
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro	
150 155 160	
ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca	591
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys	
165 170	
agaggaggga caggagaggg cctttccctg gcctttctgt cttcgttgat gttcacttcc	651
aggaacggtc tcgtgggctg ctaagggcag ttcctctgat atcctcacag caagcacagc	711
tctctttcag gctttccatg gagtacaata tatgaactca cactttgtct cctctgttgc	771
ttctgtttct gacgcagtct gtgctctcac atggtagtgt ggtgacagtc cccgagggtc	831
gacgtcotta cgggtggcgtg accagatcta cgggagagag actgagagga agaaggcagt	891
gctggagggtg cagggtggcat gtagaggggc caggccgagc atcccaggca agcatccttc	951
tgcccgggta ttaataggaa gccccatgcc gggcggctca gccgatgaag cagcagccga	1011

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gggc

2815

<210> 168

<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu
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Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
20 25 30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
35 40 45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
50 55 60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
65 70 75 80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
85 90 95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
100 105 110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
115 120 125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
130 135 140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr
145 150 155 160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
165 170

<210> 169

<211> 3337

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136).. (1755)

<400> 169

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gtg tct cca tct gtc ttc cag ccc ctg gcc cgt tcc acc ccc agg	843
Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg	
225 230 235	
gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc	891
Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr	
240 245 250	
tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag	939
Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu	
255 260 265	
ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc	987
Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser	
270 275 280	
agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc	1035
Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr	
285 290 295 300	
acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca	1083
Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro	
305 310 315	
gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc	1131
Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro	
320 325 330	
cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa	1179
Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys	
335 340 345	
ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct	1227
Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro	
350 355 360	
act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac	1275
Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp	
365 370 375 380	
ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc	1323
Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly	
385 390 395	
gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg	1371
Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg	
400 405 410	
ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta	1419
Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val	
415 420 425	
gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc	1467
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser	
430 435 440	
acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat	1515
Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr	

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563
 Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile
 465 470 475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611
 Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly
 480 485 490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659
 Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys
 495 500 505

cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggc 1707
 His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly
 510 515 520

gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac 1755
 Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
 525 530 535 540

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 ttaccgttcc agggtagctt tg 3337

<210> 170
 <211> 540
 <212> PRT
 <213> Homo sapiens

<400> 170

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 20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
 35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
 50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
 65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln
 85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
 100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
 115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
 130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
 145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
 165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
 180 185 190
 Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala
 195 200 205
 Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
 210 215 220
 Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
 225 230 235 240
 Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
 245 250 255
 Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
 260 265 270
 Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
 275 280 285
 Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
 290 295 300
 Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
 305 310 315 320
 Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
 325 330 335
 Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
 340 345 350
 Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
 355 360 365
 Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
 370 375 380
 Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
 385 390 395 400
 Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
 405 410 415
 Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
 420 425 430
 Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
 435 440 445
 Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
 450 455 460
 Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
 465 470 475 480
 Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
 500 505 510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
 515 520 525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
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<210> 171
 <211> 3579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (242).. (3094)

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 gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccc 180
 gggaaggagg cagggaaggg ccgggcttgg gggcaggtgg tccgggcatc cagccttgaa 240
 g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289
 Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
 1 5 10 15
 gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337
 Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu
 20 25 30
 atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385
 Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
 35 40 45
 ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc 433
 Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
 50 55 60
 aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc 481
 Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
 65 70 75 80
 atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac 529
 Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
 85 90 95
 ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga 577
 Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
 100 105 110

gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys 115 120 125	625
cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu 130 135 140	673
gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser 145 150 155 160	721
gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu 165 170 175	769
ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro 180 185 190	817
ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser 195 200 205	865
cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro 210 215 220	913
agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro 225 230 235 240	961
ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro 245 250 255	1009
ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu 260 265 270	1057
cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg 275 280 285	1105
gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu 290 295 300	1153
ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro 305 310 315 320	1201
gac cca ccg tca cca ccg tgc cag cct ccg acc ccc gct acg gcg ccc Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro 325 330 335	1249
tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg	1297

Ser	Thr	Thr	Glu	Val	Pro	Pro	Pro	Pro	Arg	Thr	Leu	Leu	Ala	Leu			
			340					345					350				
gag	cag	cgg	atg	gag	cgg	tac	cag	gtg	gcc	gca	gcc	cag	gcc	aag	agc	1345	
Glu	Gln	Arg	Met	Glu	Arg	Tyr	Gln	Val	Ala	Ala	Ala	Gln	Ala	Lys	Ser		
		355					360					365					
aag	ggg	gac	cag	cgg	aaa	gct	cga	atg	cac	gag	cgc	atc	gtc	aag	caa	1393	
Lys	Gly	Asp	Gln	Arg	Lys	Ala	Arg	Met	His	Glu	Arg	Ile	Val	Lys	Gln		
	370					375					380						
tac	caa	gat	gcc	atc	cga	gcc	cac	aag	gct	ggc	cga	gcc	gtg	gat	gtc	1441	
Tyr	Gln	Asp	Ala	Ile	Arg	Ala	His	Lys	Ala	Gly	Arg	Ala	Val	Asp	Val		
385					390					395					400		
gct	gaa	ttg	ccc	gtg	ccc	cca	ggc	ttc	ccc	cca	atc	cag	ggc	ctg	gag	1489	
Ala	Glu	Leu	Pro	Val	Pro	Pro	Gly	Phe	Pro	Pro	Ile	Gln	Gly	Leu	Glu		
				405					410					415			
gcc	acc	aag	ccc	acc	cag	cag	agt	ctg	gtg	ggc	gtc	ctg	gag	act	gcc	1537	
Ala	Thr	Lys	Pro	Thr	Gln	Gln	Ser	Leu	Val	Gly	Val	Leu	Glu	Thr	Ala		
			420					425					430				
atg	aag	ctg	gcc	aac	cag	gat	gaa	ggc	cca	gag	gat	gaa	gag	gat	gag	1585	
Met	Lys	Leu	Ala	Asn	Gln	Asp	Glu	Gly	Pro	Glu	Asp	Glu	Glu	Asp	Glu		
		435					440					445					
gtg	cct	aag	aag	cag	aac	agc	cct	gtg	gcc	ccc	aca	gcc	cag	ccc	aaa	1633	
Val	Pro	Lys	Lys	Gln	Asn	Ser	Pro	Val	Ala	Pro	Thr	Ala	Gln	Pro	Lys		
	450					455					460						
gcc	cca	ccc	tca	aga	act	ccc	cag	tcg	gga	tca	gcc	cca	aca	gcc	aaa	1681	
Ala	Pro	Pro	Ser	Arg	Thr	Pro	Gln	Ser	Gly	Ser	Ala	Pro	Thr	Ala	Lys		
465					470				475						480		
gcg	ccc	ccc	aaa	gcc	aca	tcc	acc	aga	gcc	cag	cag	cag	ctg	gcc	ttc	1729	
Ala	Pro	Pro	Lys	Ala	Thr	Ser	Thr	Arg	Ala	Gln	Gln	Gln	Leu	Ala	Phe		
				485					490					495			
cta	gag	ggc	cgc	aag	aag	cag	ctc	ctg	cag	gcc	gca	ctg	cga	gcc	aag	1777	
Leu	Glu	Gly	Arg	Lys	Lys	Gln	Leu	Leu	Gln	Ala	Ala	Leu	Arg	Ala	Lys		
			500					505					510				
cag	aaa	aac	gac	gtg	gag	ggc	gcc	aag	atg	cac	ctg	cgc	caa	gcc	aag	1825	
Gln	Lys	Asn	Asp	Val	Glu	Gly	Ala	Lys	Met	His	Leu	Arg	Gln	Ala	Lys		
		515					520					525					
gga	ctg	gag	cct	atg	ctg	gag	gcc	tcg	cgc	aat	ggg	ctg	cct	gtg	gac	1873	
Gly	Leu	Glu	Pro	Met	Leu	Glu	Ala	Ser	Arg	Asn	Gly	Leu	Pro	Val	Asp		
	530					535					540						
atc	acc	aag	gtg	ccg	cct	gcc	cct	gtc	aac	aag	gac	gac	ttt	gcc	ctg	1921	
Ile	Thr	Lys	Val	Pro	Pro	Ala	Pro	Val	Asn	Lys	Asp	Asp	Phe	Ala	Leu		
545					550					555					560		
gtc	cag	cgg	cct	ggc	ccg	ggc	ctg	tct	cag	gag	gcc	gcc	cgg	cgc	tat	1969	
Val	Gln	Arg	Pro	Gly	Pro	Gly	Leu	Ser	Gln	Glu	Ala	Ala	Arg	Arg	Tyr		
				565					570					575			

ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac	2017
Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn	
580 585 590	
cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag	2065
His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys	
595 600 605	
ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag	2113
Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys	
610 615 620	
caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa	2161
Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln	
625 630 635 640	
agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac	2209
Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp	
645 650 655	
atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga	2257
Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly	
660 665 670	
ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat	2305
Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr	
675 680 685	
ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac	2353
Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn	
690 695 700	
aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc	2401
Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg	
705 710 715 720	
agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc	2449
Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe	
725 730 735	
gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg	2497
Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly	
740 745 750	
aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg	2545
Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg	
755 760 765	
gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg	2593
Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu	
770 775 780	
gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag	2641
Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu	
785 790 795 800	
acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg	2689

Thr Thr Thr Glu A	805	Pro Leu Val Ile Asp Pro Val Pro	810	Ala Val	815	
ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc	2737	Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala	820	825	830	
cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc	2785	Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu	835	840	845	
agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc	2833	Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala	850	855	860	
ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac	2881	Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr	865	870	875	880
cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag	2929	Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln	885	890	895	
ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag	2977	Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln	900	905	910	
ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc	3025	Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser	915	920	925	
agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt	3073	Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser	930	935	940	
gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagccccag						3124
Glu Leu Gln Arg Leu Arg Arg						945 950
aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca						3184
gacaatcagc ggacaatcgg ttctggactc acccctcadc cgggccccca gccccgccag						3244
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aggcctggct gggccctgga gagtctgtt tgcacagccc aggggtgtcc ggcctctggc						3364
ccgccccgga gcaggagggg cggctggggc caagccccga gggcccctgc aagcacttta						3424
cttctgttc ctccccagcc ttaaccccaa agccctcctg caccctaaag aagccactga						3484
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<210> 172

<211> 951

<212> PRT
<213> Homo sapiens

<400> 172

Met	His	Lys	Arg	Lys	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Arg	Gly	Ala	Ala	
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Ala	Ala	Arg	Gln	Leu	Gly	Leu	Leu	Val	Asp	Leu	Ser	Pro	Asp	Gly	Leu	
			20					25					30			
Met	Ile	Pro	Glu	Asp	Gly	Ala	Asn	Asp	Glu	Glu	Leu	Glu	Ala	Glu	Phe	
		35					40					45				
Leu	Ala	Leu	Val	Gly	Gly	Gln	Pro	Pro	Ala	Leu	Glu	Lys	Leu	Lys	Gly	
	50					55					60					
Lys	Gly	Pro	Leu	Pro	Met	Glu	Ala	Ile	Glu	Lys	Met	Ala	Ser	Leu	Cys	
65					70					75					80	
Met	Arg	Asp	Pro	Asp	Glu	Asp	Glu	Glu	Glu	Gly	Thr	Asp	Glu	Asp	Asp	
				85					90					95		
Leu	Glu	Ala	Asp	Asp	Asp	Leu	Leu	Ala	Glu	Leu	Asn	Glu	Val	Leu	Gly	
			100					105					110			
Glu	Glu	Gln	Lys	Ala	Ser	Glu	Thr	Pro	Pro	Pro	Val	Ala	Gln	Pro	Lys	
		115					120					125				
Pro	Glu	Ala	Pro	His	Pro	Gly	Leu	Glu	Thr	Thr	Leu	Gln	Glu	Arg	Leu	
	130					135					140					
Ala	Leu	Tyr	Gln	Thr	Ala	Ile	Glu	Ser	Ala	Arg	Gln	Ala	Gly	Asp	Ser	
145					150				155						160	
Ala	Lys	Met	Arg	Arg	Tyr	Asp	Arg	Gly	Leu	Lys	Thr	Leu	Glu	Asn	Leu	
				165					170					175		
Leu	Ala	Ser	Ile	Arg	Lys	Gly	Asn	Ala	Ile	Asp	Glu	Ala	Asp	Ile	Pro	
		180						185					190			
Pro	Pro	Val	Ala	Ile	Gly	Lys	Gly	Pro	Ala	Ser	Thr	Pro	Thr	Tyr	Ser	
		195					200						205			
Pro	Ala	Pro	Thr	Gln	Pro	Ala	Pro	Arg	Ile	Ala	Ser	Ala	Pro	Glu	Pro	
	210					215					220					
Arg	Val	Thr	Leu	Glu	Gly	Pro	Ser	Ala	Thr	Ala	Pro	Ala	Ser	Ser	Pro	
225					230					235					240	
Gly	Leu	Ala	Lys	Pro	Gln	Met	Pro	Pro	Gly	Pro	Cys	Ser	Pro	Gly	Pro	
				245					250					255		
Leu	Ala	Gln	Leu	Gln	Ser	Arg	Gln	Arg	Asp	Tyr	Lys	Leu	Ala	Ala	Leu	
			260					265					270			
His	Ala	Lys	Gln	Gln	Gly	Asp	Thr	Thr	Ala	Ala	Ala	Arg	His	Phe	Arg	
		275					280					285				

Val Ala Lys Ser Pro Asp Ala Val Leu Glu Ala Leu Ser Gly Glu
 290 295 300
 Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro
 305 310 315 320
 Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
 325 330 335
 Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
 340 345 350
 Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
 355 360 365
 Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
 370 375 380
 Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
 385 390 395 400
 Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
 405 410 415
 Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
 420 425 430
 Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
 435 440 445
 Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
 450 455 460
 Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
 465 470 475 480
 Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
 485 490 495
 Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
 500 505 510
 Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
 515 520 525
 Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
 530 535 540
 Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
 545 550 555 560
 Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
 565 570 575
 Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
 580 585 590
 His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys

Phe	Glu	Lys	Leu	Ala	Glu	Asp	Cys	Lys	Arg	Ser	Met	Asp	Ile	Leu	Lys
610						615					620				
Gln	Ala	Phe	Val	Arg	Gly	Leu	Pro	Thr	Pro	Thr	Ala	Arg	Phe	Glu	Gln
625					630					635					640
Arg	Thr	Phe	Ser	Val	Ile	Lys	Ile	Phe	Pro	Asp	Leu	Ser	Ser	Asn	Asp
				645					650					655	
Met	Leu	Leu	Phe	Ile	Val	Lys	Gly	Ile	Asn	Leu	Pro	Thr	Pro	Pro	Gly
			660					665					670		
Leu	Ser	Pro	Gly	Asp	Leu	Asp	Val	Phe	Val	Arg	Phe	Asp	Phe	Pro	Tyr
		675					680					685			
Pro	Asn	Val	Glu	Glu	Ala	Gln	Lys	Asp	Lys	Thr	Ser	Val	Ile	Lys	Asn
	690					695					700				
Thr	Asp	Ser	Pro	Glu	Phe	Lys	Glu	Gln	Phe	Lys	Leu	Cys	Ile	Asn	Arg
705					710					715					720
Ser	His	Arg	Gly	Phe	Arg	Arg	Ala	Ile	Gln	Thr	Lys	Gly	Ile	Lys	Phe
				725					730					735	
Glu	Val	Val	His	Lys	Gly	Gly	Leu	Phe	Lys	Thr	Asp	Arg	Val	Leu	Gly
			740					745					750		
Thr	Ala	Gln	Leu	Lys	Leu	Asp	Ala	Leu	Glu	Ile	Ala	Cys	Glu	Val	Arg
		755					760					765			
Glu	Ile	Leu	Glu	Val	Leu	Asp	Gly	Arg	Arg	Pro	Thr	Gly	Gly	Arg	Leu
	770					775					780				
Glu	Val	Met	Val	Arg	Ile	Arg	Glu	Pro	Leu	Thr	Ala	Gln	Gln	Leu	Glu
785					790					795					800
Thr	Thr	Thr	Glu	Arg	Trp	Leu	Val	Ile	Asp	Pro	Val	Pro	Ala	Ala	Val
				805					810					815	
Pro	Thr	Gln	Val	Ala	Gly	Pro	Lys	Gly	Lys	Ala	Pro	Pro	Val	Pro	Ala
			820					825					830		
Pro	Ala	Arg	Glu	Ser	Gly	Asn	Arg	Ser	Ala	Arg	Pro	Leu	His	Ser	Leu
		835					840					845			
Ser	Val	Leu	Ala	Phe	Asp	Gln	Glu	Arg	Leu	Glu	Arg	Lys	Ile	Leu	Ala
	850					855					860				
Leu	Arg	Gln	Ala	Arg	Arg	Pro	Val	Pro	Pro	Glu	Val	Ala	Gln	Gln	Tyr
865					870					875					880
Gln	Asp	Ile	Met	Gln	Arg	Ser	Gln	Trp	Gln	Arg	Ala	Gln	Leu	Glu	Gln
				885					890					895	
Gly	Gly	Val	Gly	Ile	Arg	Arg	Glu	Tyr	Thr	Ala	Gln	Leu	Glu	Arg	Gln
			900					905					910		

Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
 915 920 925
 Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
 930 935 940
 Glu Leu Gln Arg Leu Arg Arg
 945 950

<210> 173
 <211> 2796
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 173
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 tagtccttaa caaagggaaa gcgataaatg taaataagct cacattttca gaatgagcgg 180
 tttgcagtaa ggagctgcgg cagcccagag tctgctcttt ttgggctggg ctaacctttc 240
 cctgtttttt gttttttgtt ttgttttgtt tttgtttttt atggataaaa atatgcgctt 300
 ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360
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 ctccagaaaa ttcatlgatt atccaagtct cagataaatc tggtgccaga gtttggtttg 480
 aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaaccctt 540
 gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594
 Met Gly Asp Arg Arg Phe Ile
 1 5
 gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga 642
 Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly
 10 15 20
 aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690
 Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr
 25 30 35
 aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738
 Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile
 40 45 50 55
 acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga 786
 Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg

agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt	834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu	
75 80 85	
ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac	882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His	
90 95 100	
tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc	930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu	
105 110 115	
acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat	978
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp	
120 125 130 135	
cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc	1026
Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr	
140 145 150	
agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc	1074
Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu	
155 160 165	
agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat	1122
Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn	
170 175 180	
gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca	1170
Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr	
185 190 195	
tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att	1218
Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile	
200 205 210 215	
cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc	1266
Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu	
220 225 230	
cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg	1314
Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val	
235 240 245	
ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta	1362
Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val	
250 255 260	
cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc	1410
Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala	
265 270 275	
att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att	1458
Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile	
280 285 290 295	

acc ttg tgc ctt gca ctg aat tgt tgc ttt gat cct ttc tat 1506
 Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr
 300 305 310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat 1554
 Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His
 315 320 325

ata agg atg gag tgc ctg ttt aag act gag aca cct ctg acc ccc aaa 1602
 Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys
 330 335 340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat 1650
 Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn
 345 350 355

aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703
 Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe
 360 365 370

caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763
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<210> 174
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 174

Met	Gly	Asp	Arg	Arg	Phe	Ile	Asp	Phe	Gln	Phe	Gln	Asp	Leu	Asn	Ser	1	5	10	15
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Val	Asp	Asp	Ser	Phe	Lys	Tyr	Asn	Leu	Asn	Gly	Ala	Val	Tyr	Ser	Val	35	40	45	
Val	Phe	Ile	Leu	Gly	Leu	Ile	Thr	Asn	Ser	Ala	Ser	Leu	Phe	Val	Phe	50	55	60	
Cys	Phe	Arg	Met	Lys	Met	Arg	Ser	Glu	Thr	Ala	Thr	Phe	Ile	Thr	Asn	65	70	75	80
Leu	Ala	Leu	Ser	Asp	Leu	Leu	Phe	Val	Cys	Thr	Leu	Pro	Phe	Lys	Ile	85	90	95	
Phe	Tyr	Asn	Phe	Asn	Arg	His	Trp	Pro	Phe	Gly	Asp	Thr	Leu	Cys	Lys	100	105	110	
Ile	Ser	Gly	Thr	Ala	Phe	Leu	Thr	Asn	Ile	Tyr	Gly	Ser	Met	Leu	Phe	115	120	125	
Leu	Thr	Cys	Ile	Ser	Val	Asp	Arg	Phe	Leu	Ala	Ile	Val	Tyr	Pro	Phe	130	135	140	
Arg	Ser	Arg	Thr	Ile	Arg	Thr	Arg	Arg	Asn	Ser	Ala	Ile	Val	Cys	Ala	145	150	155	160
Gly	Val	Trp	Ile	Leu	Val	Leu	Ser	Gly	Gly	Ile	Ser	Ala	Ser	Leu	Phe	165	170	175	
Ser	Thr	Thr	Asn	Val	Asn	Asn	Ala	Thr	Thr	Thr	Cys	Phe	Glu	Gly	Phe	180	185	190	
Ser	Lys	Arg	Val	Trp	Lys	Thr	Tyr	Leu	Ser	Lys	Ile	Thr	Ile	Phe	Ile	195	200	205	
Glu	Val	Val	Gly	Phe	Ile	Ile	Pro	Leu	Ile	Leu	Asn	Val	Ser	Cys	Ser	210	215	220	
Ser	Val	Val	Leu	Arg	Thr	Leu	Arg	Lys	Pro	Ala	Thr	Leu	Ser	Gln	Ile	225	230	235	240
Gly	Thr	Asn	Lys	Lys	Lys	Val	Leu	Lys	Met	Ile	Thr	Val	His	Met	Ala	245	250	255	
Val	Phe	Val	Val	Cys	Phe	Val	Pro	Tyr	Asn	Ser	Val	Leu	Phe	Leu	Tyr	260	265	270	

Ala Leu Val Arg Ser ████ n Ala Ile Thr Asn Cys Leu Leu ████ Arg Phe
 275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
 290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
 305 310 315 320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
 325 330 335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
 340 345 350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
 355 360 365

Thr Phe
 370

<210> 175
 <211> 2299
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (67).. (1176)

<400> 175
 cctaccggtc catagtgtca gagggtgaa cccctgcagc cagcaggcct cctgaaaaaa 60

aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca 108
 Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser
 1 5 10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156
 Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr
 15 20 25 30

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204
 Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr
 35 40 45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252
 Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe
 50 55 60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300
 Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
 65 70 75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348
 Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
 80 85 90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc	396
Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu	
95 100 105 110	
tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg	444
Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met	
115 120 125	
ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat	492
Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr	
130 135 140	
cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg	540
Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val	
145 150 155	
tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct	588
Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser	
160 165 170	
ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa	636
Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu	
175 180 185 190	
ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata	684
Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile	
195 200 205	
ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct	732
Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser	
210 215 220	
tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct	780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser	
225 230 235	
caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat	828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His	
240 245 250	
atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc	876
Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe	
255 260 265 270	
ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa	924
Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu	
275 280 285	
aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg	972
Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu	
290 295 300	
aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt	1020
Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe	
305 310 315	
cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt	1068

Gln Lys Ser Phe Tyr Leu Asn Ala His Ile Arg Met Glu Ser Leu Phe
 320 325 330

aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa 1116
 Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln
 335 340 345 350

gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta 1164
 Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu
 355 360 365

gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc 1216
 Glu Ser Thr Phe
 370

ctataatttt tccatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaattcca gtcagatata tttgtttgaa ggtatactgt agagttttta ttgctgtttt 1336

gttcagtaat tatagggtcaa atctaattac aacaaccaag atggattgcc aaactcttct 1396

gcttggttgg aatttcattg tatcgcatata tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaagggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttggactg tcattgagtt tatttttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgtta 1696

tgtgcatttt gaaaacagaa acaaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcgtt 1816

gtttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gccaggtca ggagcaaatt gaaaaaaaa ataaagtaat actaaaaaat 2116

caaaactataa acccaaaaaca tttattaaaa cctgaattaa tccttttttg aggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236

caggagctgc tgaatttgtg cccctggatt ggaaccaaatt aaaaaaaaa aaaaaaaatt 2296

cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser
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Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
20 25 30
Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
35 40 45
Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe
50 55 60
Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
65 70 75 80
Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
85 90 95
Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
100 105 110
Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
115 120 125
Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
130 135 140
Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145 150 155 160
Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
165 170 175
Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
180 185 190
Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
195 200 205
Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
210 215 220
Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225 230 235 240
Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
245 250 255
Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
260 265 270
Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
275 280 285
Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
 305 310 315 320
 Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
 325 330 335
 Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
 340 345 350
 Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
 355 360 365
 Thr Phe
 370

<210> 177
 <211> 973
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (30).. (416)

<400> 177
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 Met Ala Arg Gly Ser Leu Arg Arg
 1 5
 ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 101
 Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
 10 15 20
 gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149
 Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
 25 30 35 40
 tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197
 Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
 45 50 55
 gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245
 Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
 60 65 70
 gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293
 Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
 75 80 85
 acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341
 Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
 90 95 100
 cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389
 Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgccca 436
 Gly Cys Pro Ala Val Ala Leu Ile Gln
 125

gccggggctc gccactcat cattcattca tccattctag agccagtctc tgcctcccag 496
 acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcgggtg aatcacctcc 556
 gaggcctggg tccagggttc aggggaacct tccaagggtg ctggttgccc tgcctctggc 616
 tccagaacag aaaggagacc tcacgctggc tcacacaaaa cagctgacac tgactaagga 676
 actgcagcat ttgcacaggg gaggggggtg cctccttcc tagaggccct gggggccagg 736
 ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac 796
 cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggcccacta 856
 ggagggtg ccctaagata cagaccccc caactcccca aagcggggag gagatattta 916
 ttttggggag agtttggagg ggaggagaa tttattaata aaagaatctt taacttt 973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
 1 5 10 15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
 65 70 75 80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
 85 90 95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 100 105 110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
 115 120 125

Gln

<210> 179
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 179
cttctgctct aaaagctgcg 20

<210> 180
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 180
cgacctgcag ctcgagcaca 20

FREE TEXT OF SEQUENCE LISTING

SEQ ID NO: 179 and SEQ ID NO: 180 are primers.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a graph showing NF- κ B reporter activity inhibition by the proteasome inhibitor MG132 in Example 3, the axis of abscissa is MG132 concentration and the transversal axis is relative luciferase activity.

NAME OF THE DOCUMENT: ABSTRACT

ABSTRACT

PROBLEMS TO BE SOLVED: Provision of proteins having NF- κ B activity, which are used for diagnosing, treating or preventing diseases associated with the excessive activation or inhibition of NF- κ B.

MEANS TO SOLVE THE PROBLEMS: Using the plasmid pNF κ B-Luc, the cDNA encoding a protein capable of activating NF- κ B has been cloned from the cDNA library constructed from human lung fibroblasts, and the DNA sequence and the deduced amino acid sequence determined. The protein, the DNA encoding the protein, a recombinant vector containing the DNA, and a transformant containing the recombinant vector are useful for screening a substance inhibiting or promoting NF- κ B activation.

FIG.1

